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February 10, 2004, 16:18:30; Search time 11.5063 Seconds (without alignments) 731.761 Million cell updates/sec
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                                                                                                                                                             US-10-083-336A-5
1025
1 MIPPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 199
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Patent No. 52
Sequence 16,
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Sequence 1,
Sequence 27,
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l. /cgn2 6/ptodata//iaa/5A COMB.pep:*
s: /cgn2 6/ptodata//iaa/5B-COMB.pep:*
f. /cgn2 6/ptodata/1/iaa/6A COMB.pep:*
f. /cgn2 6/ptodata/1/iaa/6B COMB.pep:*
s: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
s: /cgn2 6/ptodata/1/iaa/PCTUS COMB.pep:*
c/cgn2 6/ptodata/1/iaa/Packfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-218-303-16
US-08-338-793D-61
US-09-538-873-1
US-08-485-286-77
US-08-488-113B-6
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-488-113B-1
US-08-446-113B-1
US-08-646-366-1
US-08-839-765-1
US-09-136-389-1
US-09-610-888-1
PCT-US92-09487-1
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US-08-485-286-27
5248606-4
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                                                                                                                                                                                                                                                                              328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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US-08-485-286-74	US-07-923-692C-4	US-08-184-237-4	US-08-482-920-4	US-08-484-341-4	US-08-483-502-4	US-09-726-651A-4	US-08-324-301-15	US-08-378-761A-71	US-08-485-286-71	US-09-538-873-3	US-07-901-707-6	US-07-988-430-6	US-08-425-336-6	PCT-US92-09487-6	US-08-902-486-7	US-08-245-754A-2	US-08-597-731-2	
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267	289	289	289	289	289	289	282	250	250	251	255	255	255	255	248	290	290	
33.4	33.4	33.4	33.4	33.4	33.4	33.4	33.3	32.1	32.1	31.6	30.5	30.5	30.5	30.5	30.4	30.4	30.4	
342	342	342	342	342	342	342	341.5	329.5	329.5	323.5	312.5	312.5	312.5	312.5	312	312	312	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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APPLICANT: Huston, James S.
APPLICANT: Huston, Lamann, Hermann, APPLICANT: Oppermann, Hermann, APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 02109

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 1025; DB 2;
Best Local Similarity 100.0%; Pred. No. 6e-112;
Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PItcher; Redmind R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEC 1D NO: 8:
                          Sequence 8, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 268 amino acids TYPE: amino acid
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LENGTH: 268 amino aci
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                                                                                      GENERAL INFORMATION
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US-08-356-786-8
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Length 268; Indels

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VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAF 120
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                                                                                                                                                                    121 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 180
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  MIFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL
                                     1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL
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Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 199; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
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REPERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5877305
                                                                                                                                                                                                                                                                                      181 RFOYIEGEMRIRIRYNRRS 199
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INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CENERAL INFORMATION: James S. APPLICANT: Huston, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/83
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-356-786-10
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61 VELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNOEDAEAITHLFTDVQNRYTFAF 120

3 MIPPKQYPIINFTIAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRPIL 62

1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL

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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
                                                                             121 GGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAA 180
63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
                                                                                                                                       181 RFQYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                     183 RPOYIEGEMRTRIRYNRRS 201
                                                                                                                                                                                                                                                                             US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19920619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein US-07-901-707-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicago
: Illinois
RY: USA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60603
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SOFTWARE: Patentin Ver. 2.1
                                             SEQ ID NO 1
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APPLICANT: GHETTE, VICTOR F.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: GHETTE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REPERENCE: UTSD: 884US
CURRENT PELLING DATE: 2002-10-29
FRIOR RILING DATE: 2000-03-30
FRIOR PRILING DATE: 2000-03-30
FRIOR FILING DATE: 1999-03-30
FRIOR FILING DATE: 2091-03-30
FRIOR FILING DATE: 2001-03-30
FRIOR FILING DATE: 2001-03-30
FRIOR FILING DATE: 2091-03-30
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FRIOR FILING
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APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FILE REFERENCE: UTSD:603
CURRENT APPLICATION NUMBER: US/10/440,796
PRIOR PILING DATE: 2003-05-19
PRIOR PLICATION NUMBER: US/09/538,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 1019; DB 12; Length 267; Best Local Similarity 100.0%; Pred. No. 2.2e-108; Matches 198; Conservative 0; Mismatches 0; Indels 0;
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PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
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US-10-282-935-1
; Sequence 1, Application US/10282935

Publication No. (US2030143193A1
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Publication No. US20040009148A1
GENERAL INFORMATION:
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APPLICANT: VITETTA, ELLEN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-935-1
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GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Mannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: PS7452USG (RIID 01-58)
CURRENT APPLICATION NUMBER: US110/083,336A
                                                                                                                                                                                                                                                                                                                 1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                  OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
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99.1%; Score 1010; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-107;
Matches 196; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                         Best Local Similarity 100.0
Matches 198; Conservative
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US-10-083-336A-3
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Matches 200; Conservative
                                                                 February 10, 2004, 16:18:30; Search time 11.5641 Seconds (without alignments) 731.761 Million cell updates/sec
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Sequence,27, 7
Patent No. 5248
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-488-430-1
US-08-428-336-1
US-08-488-113B-1
US-08-47-484B-1
US-08-646-360-1
US-08-639-765-1
US-09-610-638-1
US-09-610-638-1
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US-08-338-793D-61
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US-08-485-286-27
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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sednence Sed	for Cancer & Thibeault	4
28 342 33.2 267 1 US-08-485-286-74 29 342 33.2 289 1 US-07-923-692C-4 31 342 33.2 289 1 US-07-923-692C-4 33 342 33.2 289 1 US-08-184-237-4 33 342 33.2 289 3 US-08-484-341-4 34 34.2 33.2 289 3 US-08-48.341-4 35 34.2 33.2 289 3 US-08-48.3-502-4 35 34.2 33.2 289 3 US-08-48.3-502-4 35 329.5 32.0 289 1 US-08-328-301-15 36 329.5 32.0 250 1 US-08-328-301-15 38 329.5 31.4 255 1 US-07-901-707-6 40 312.5 30.4 255 1 US-07-901-707-6 41 312.5 30.4 255 1 US-07-908-450-6 42 312 30.3 248 3 US-08-425-338-6 44 312 30.3 248 3 US-08-922-486-7 45 312 30.3 290 1 US-08-925-548.7	ALIGNMENTS 1	Similarity 100.0%; Pred. No. 2.2e-10; Conservative 0; Mismatches

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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
WUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                            123 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ELSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SOFTWARE:
SOFTWARE:
PALCATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
FION APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: US 07/787,567
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                         181 RFQYIEGEMRTRIRYNRRSA 200
                                                                                                                                                                    183 RFQYIEGEMRIRIRYNRRSA 202
                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/07901707; Patent No. 5376546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (312) 346-5750 TELEFAX: (312) 984-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 267 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
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Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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CITY: C
STATE:
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                                                                                         61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                                                       61 VELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAF 120
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                           1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
MIPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                181 RFQYIEGEMRTRIRYNRRSA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pitcher, Edmund R. REGISTRAITON NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 amino acids
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Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-356-786-10
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COUNTRY:

LENGTH:

Query Match

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

February 10, 2004, 16:17:35 ; Search time 10.7687 Seconds

(without alignments) 1777.145 Million cell updates/sec

US-10-083-336A-5 1025 Title: Perfect score: Sequence:

1 MIFPKQYPIINFTTAGATVQ.......ARFQYIEGEMRTRIRYNRRS 199

BLOSUM62 Scoring table:

283308 seqs, 96168682 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ω		ricin D precursor	. :	abrin-d precursor			- 17	karasurin - Mongol	8	karasurin C - Tric	abrin (clone 7.2)			BE	in	mistletoe lectin I	rRNA N-glycosidase			rRNA N-qlycosidase	rRNA N-qlycosidase	rRNA N-glycosidase	rRNA N-glycosidase		antiviral protein	rRNA N-glycosidase	betavulgin - beet	rRNA N-qlycosidase	rRNA N-glycosidase	tritin - wheat
SUMMARIES																														
SUM	ΙD	RLCSD	RLCSAG	532431	S16022	532430	RLTZT	JU0393	JC5032	JC5606	C39761	TZLSA	823519	JN0108	862627	PD0018	522494	825560	JC4840	RLPUGG	JC4235	JT0753	528421	517757	JE0401	A39817	JC4811	T12573	RLBH	833631
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	Length	576	564	528	562	527	289	247	247	289	251	528	278	250	570	254	277	286	245	286	286	316	294	313	261	278	272	289	280	275
obe	Query	l On	0		34.5				33.0	33.0		32.1	30.0	29.3	28.4			27.2	27.1		26.5		19.3	17.8	17.6	•	'n		13.7	13.4
	Score	-	3	353.5	ß	345	342	338	338	338	336.5	329.5	307.5	300.5	291		284.5	279	278	277	272	242.5	197.5	182	180.5	178	156	149.5	4	137
	Result No.		7	М	4	S	φ	7	6 0	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

30K ribosome inact	protein synthesis	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	shiga-like toxin I	Shiga toxin 2 subu	Shiga toxin 2 subu	Shiga-like toxin I	rRNA N-glycosidase				
B38664	JC5848	S28542	S28539	S29931	S46239	S05205	S17519	S28541	RLQHG2	A58923	I54695	E90779	G85640	801032	S17932
7	7	N	7	7	N	N	7	~	н	7	7	7	7	N	0
281	280	253	253	253	310	283	293	253	292	253	319	319	319	318	236
13.0	12.9	12.8	12.4	12.4	12.3	12.1	12.0	12.0	11.8	11.2	10.8	10.8	10.8	10.8	10.7
133	132	131	127	127	126	124	123.5	123	121	115	111	111	111	110.5	110
0	ᅼ	2	33	34	35	96	37	88	39	9	디	2	£	4	rī.

ALIGNMENTS

ricin D precursor - castor bean Nicontains rRNA N-Glycosidase (EC 3.2.2.2) C;Species: Ricinus communis (castor bean) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999 C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903 C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903 R;Halling, K.C.; Halling, A.C.; Wurray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8033, 1985 A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041 A;Molecule type: DNA A;Residues: 1-576 cHAL> A;Molecule type: DNA A;Residues: 1-576 cHAL> A;Cross_references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18 515-525, 1992 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1371405	RESUL	KESULT 1
N; Contains: rRNA N-glycosidase (EC 3.2.22) C; Species: Ricinua communis (castor bean) C; State: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999 C; Accession: A24041; S20513; Ā24614; A03372; A24010; A03374; S10903 R; Halling, X.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8013, 1985 A; Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A; Reference number: A24041 A; Molecule type: DNA A; Residues: 1-576 cHAL> A; Residues: 1-576 cHAL> A; Residues: 1-576 cHAL> A; Cross-references: GB:X01179; NID:g21082; PIDN:CAA26939.1; PID:g21083 B; Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a A; Reference number: S20513; MulD:92163016; PMID:1371405	ric	in D precursor - castor bean
C;Species: Ricinus communis (castor bean) C;Species: Ricinus communis (castor bean) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999 C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903 R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8033, 1985 A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041 A;Reference number: A24041 A;Molecule type: DNA A;Residues: 1-576 cHAL> A;Residues: 1-576 cHAL> A;Residues: 1-576 cHAL> A;Residues: 1-576 cHAL> A;Residues: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A;Tresgear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a A;Reference number: S20513; MulD:92163016; PMID:1371405	N, N	ontains: rRNA N-glycosidase (EC 3.2.2.22)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999 C;Accession: A24041, S20513, A24614; A03372; A24010; A03374; S10903 R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8033, 1985 A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041 A;Molecule type: DNA A;Residues: 1-576 cHAL. A;Coss.references: GB:X01179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Ttle: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:921616; PMID:1371405	3,5	pecies: Ricinus communis (castor bean)
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; \$10903 R;Halling, K.C; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8013, 1985 A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041 A;Molecule type: DNA A;Residues: 1-576 cHAL> A;Cross-references: GB:X013179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MulD:9216016; PMID:1371405	C;I	ate: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F. Nucleic Acids Res. 13, 8019-8033, 1985 A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041; MUID:86067214; PMID:2999712 A;Recession: A24041 A;Molecule type: DNA A;Residues: 1-576 cHML> A;Residues: 1-576 cHML> A;Residues: 1-576 cHML> A;Residues: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A;Tresgear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Title: The lectin gene Eamily of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1371405	4,5	ccession: A24041; S20513; A24614; A03372: A24010; A03374; S10903
Nucleic Acids Res. 13, #019-8033, 1985 A,Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A,Reference number: A24041; MUID:86067214; PMID:2999712 A;Recession: A24041 A;Molecule type: DNA A;Residues: 1-576 c.HAL. A;Cross-references: GB:X03179; NID:921082; PIDN:CAA26939.1; PID:921083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1997 A;Ritle: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1371405	R;E	alling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis. A;Reference number: A24041; MUID:86067214; PMID:2999712 A;Accession: A24041 A;Molecule type: DNA A;Residues: 1-576 c4HAL> A;Residues: 1-576 c4HAL> A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1997 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1371405	Nuc	leic Acids Res. 13, 8019-8033, 1985
A; Reference number: A24041; MUID:86067214; PMID:2999712 A; Accession: A24041 A; Molecule type: DNA A; Residues: 1-576 cHAL> A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A; Tresgear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A; Title: The lectin gene Eamily Of Ricinus communis: cloning of a functional ricin gene & A; Reference number: S20513; MUID:92163016; PMID:1371405	A;1	itle: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A;Accession: A24041 A;Molecule type: DNA A;Residues: 1-576 <all> A;Residues: 1-576 <all> A;Coss-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 B;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Ritle: The lectin gene samily of Ricinus pwiD:1371405</all></all>	A;F	eference number: A24041; MUID:86067214; PMID:2999712
A; Molecule type: DNA A; Residues: 1-576 - 4NAL> A; Residues: 1-576 - 4NAL> A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A; Cross-references: B. X. M. Roberts, L. M. R. Tregear, J. W.; Roberts, L. M. R. Plant Mol. Biol. 18, 515-525; 1992 A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a A; Reference number: S20513; MUID:92165016; PMID:1371405	A;4	ccession: A24041
A; Residues: 1-576 <hal> A; Rossidues: 05.70 (HAL) A; Cross-references: 05.701179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A; Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene fakterence number: S20513; MUID:92165016; PMID:1371405</hal>	A;N	olecule type: DNA
A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R; Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A; Reference number: S20513; MUID:92165916; PMID:1371405	A;E	esidues: 1-576 <hal></hal>
R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 195 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1371405	A;C	ross-references: GB:X03179; NID:q21082; PIDN:CAA26939.1; PID:q21083
Plant Mol. Biol. 18, 515-525, 1992 A,Title: The lectin gene Eamily Of Ricinus communis: cloning of a functional ricin gene & A,Reference number: S20513; MUID:92163016; PMID:1371405	R;1	regear, J.W.; Roberts, L.M.
A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a A;Reference number: \$20513; MUID:92163016; PMID:1371405	Pla	nt Mol. Biol. 18, 515-525, 1992
A; Reference number: S20513; MUID:92163016; PMID:1371405	A;1	itle: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a
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A;kererence number: 520: A;Accession: 520513 A;Molecule type: DNA A;Residues: 1-576 <TRE>

A; Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085 R; Lamb, F.I.; Roberts, L.M.; Lord, J.M.
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
A; Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A; Reference number: A24614; MuID:85179479; PMID:3838723
A; Accession: A24614

A; Molecule type: mRNA A; Residues: 12-75, D', 77-550, R', 552-576 <LAM> A; Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 A; Yoshitake, S.; Funatsu, G.; Funatsu, M. Agric, Biol. Chem. 42, 1267-1274, 1978 A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile chata, A; Reference number: A03372 A; Accession: A03372

A; Molecule type: protein
A; Molecule type: protein
A; Residues: 36-97, (0', 99-109, '8', 111-269, 'D', 272-283, 'L', 285-288, 290-302 < YOS>
A; Note: this paper cites the others in the series providing experimental details for the R; Araki, T.; Funatsu, G.
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A; FESS Lett. 191, 121-124, 1985
A; Title: Revised amina acid sequence of the B-chain of ricin D due to loss of tryptophan A; Reference number: A24010

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A Molecule type: protein
A; Residues: 315-383, PS', 386-576 < ARA>
A; Residues: 315-383, PS', 386-576 < ARA>
B; Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A; Title: Primary structure of Ala chain of ricin D.
A; Reference number: A03374
A; A; Acession: A03374
A; Molecule type: protein

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A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40
527,'E',529-564''W',566,'H',567-570,'LI',573-574,'F' <FUNS
A;Note: this paper, one of a series, summarizes the experimental details for the determinence and the proteins 10, 270-278, 1991
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of A;Reference number: A48231 MUID:91352006; PMID:1881883
A;Contents: annotation, active site
Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; MUID:91352005; PMID:1881882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Contents: annotation; X-ray crystallography, 2.5 angstroms
A/Contents: annotation; X-ray crystallography, 2.5 angstroms
C/Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C/Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C/Comment: The A chain; B chains are also responsible for cell agglutination (lectic comment: This protein is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/Superfamily: ricin is cytotoxic and very poisonous to animals.
C/SUPERFAMILY: ricin D chain A #status experimental <ACH>
C/SCAPACOMANIN: TRNA N-Glycosidase homology <ARNOS-
C/SUPERFAMILY: All 4/17-455, 462-440, 543-576 (Region: 40-residue repeats)
C/SUPERFAMILY: All 4/14, 417-455, 462-440, 543-576 (Region: 40-residue repeats)
C/SUPERFAMILY: All 4/14, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 417-455, 41
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CiSpecies: Ricinus communis (castor bean)
CiAccession: A24261; A24210
C;Rocersion: A24261; A24210
C;Rocersion: A24261; A24210
C;Rocersion: A24261; A24210
C;Rocersion: A24261; A24210
C;Rocerts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
A;Reference number: A24261, MUID:86059449; PMID:2999130
A;Recente type: mRNA
A;Residues: 1-564 RNBA
A;Residues: 1-564 RNBA
A;Residues: 1-564 RNBA
A;Residues: 1-564 RNBA
A;Cross-references: GB:MI2089; NID:9169700; PIDN:AAA33869.1; PID:9169701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Concents: annotation; X-7; crystallography, 2.5 angstroms R; Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A; Title: Structure of ricin A-chain at 2.5 angstroms.
A; Reference number: A48239; MUID:91352004; PMID:1881881
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein has strong agglutinating activity and weak cytotoxicity compared
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C;Guperfamily: richi, FRNA N-91yCosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
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F;35-29/Droduct: agglutinin chain A #status predicted <ACH>
F;35-29/Product: agglutinin chain B #status predicted <ACH>
F;35-29/Product: agglutinin chain B #status experimental <BCH>
F;35-29/Product: agglutinin chain B #status predicted
F;30-364/Product: agglutinin chain B #status predicted
F;30-364/Product: agglutinin glie: substrate (Apr) (covalent) #status predicted
F;30-364/Product: agglutinin glie: substrate (Apr) (covalent) #status predicted
F;20,203/Active site: Glu, Agg #status predicted
F;20,203/Active site: Glu, Agg #status predicted
F;282-306,332-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F;34,337,349/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted
F;356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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S;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993 A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Co A;Reference number: S32429; MUID:93132798; PMID:8421313
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F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-d chain B #status predicted <BCH>
R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GNYDRIEQL-GGLRENIELGTGPLEDAISALYYYSTCGTQIPTLARSFMVCIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 IFPKQYPIINFTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 ELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.8%; Score 930.5; DB 1;
91.9%; Pred. No. 5.6e-76;
live 7; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abrin-d precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hung, C.; Lee, M.; Lee, T.; Lin, J. submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 FQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 FQYIEGEMRTRIRYNRRS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.94
Matches 182; Conservative
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A;Cross-references: GB:M98346
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                                                                                                                            A; Reference number: A24210
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A; Residues: 1-528 <HUN>
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                                                                                                                                                                      A; Accession: A24210
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A, Molecule type: protein
A, Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
A, Experimental source: seed
A, Experimental source: seed
C, Superfamily: ricin; rRNA N-glycosidase homology
C, Superfamily: ricin; rRNA N-glycosidase homology
C, Reywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; py
F,1-250/Product: abrin-b chain A #status predicted <ACH>
F,245/Domain: rRNA N-glycosidase homology <ANG>
F,226/Domain: rRNA N-glycosidase homology <ANG>
F,260-527/Product: abrin-b chain B #status experimental <BCH>
F,282-224,325-365,368-406,413-448,452-491,494,527/Region: 40-residue repeats
F,140/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F,14,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F,163,166/Active site: Glu, Arg #status predicted
F,163,166/Active site: Glu, Arg #status predicted
F,246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A,Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M98345; NID:gl66296; PIDN:AAA32625.1; PID:gl66297
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biscit. Biotechnol. Biochem. S7. 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                   149 DLERWAHQTREEISLGLOALTHAIS---FLRSGASNDEEKARTLIVIIOMASEAARYRYI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 SDTESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                N.Contains: rRNA N-glycosidase (EC 3.2.2.2)
C.Species: Abrus precatorius (Indian licorice)
C.Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.7%; Score 345; DB 2; Length 52.45.5%; Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                       abrin-b precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: $32430; JC1399
R,Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
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                                                                                                                                                                                                                                                206 SNRVGVSIR 214
                                                                                                                                                                                     186 EGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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A; Residues: 1-527 <HUN>
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Bur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chai
A;Reference number: S16022; MUID:91266957; PMID:2050149
A;Accession: S16022
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F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;260,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;286,286-305,239-346,417-430,486-473/Pisulfide bonds: #status predicted
F;288,312/Binding site: N-acety1galactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acety1galactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SERESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASIYLFPGTQ-RYSLRFDGSYG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
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C;Species: Abrus precarcitus (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S16022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDQVIKFTTBGATSQSYKQFIBALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 QYPIINFITAGATVQSYTNFIRAVRGRLFTGADVRHEIPVLPNRVGLPINQRFILVELSN
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                                                                                                                                                                                                                                                                                                                                                                                 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X55667; NID: 916084; PIDN: CAA39202.1; PID: 916085
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                                                                                                                                                                                                                                                                                                        ; Score 353.5; DB 2; Length 528;
; Pred. No. 5.2e-24;
24; Mismatches 70; Indels 9.
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                                                                                                                                                                                                                                                                                                               34.5%;
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Matches 86; Conserv
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- Mongolian

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C,Accession: JC5032
K, Stondo, T.; Makeni, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A,Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A,Reference number: JC5032; WUID:97108848; PMID:8951169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: TU0393; PS0163 — R;TOyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y. Chem. Pharm. Bull. 39, 1244-1249, 1991 — A;Title: The complete amino acid sequence of an abortifacient protein, karasurin. A;Reference number: JU0393; WUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                                                               S2 IISVAIDVINVYIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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                                                                                                                                                                                  25 VSFRLSGATSSSYGVEISNIRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            karasurin - Mongolian snake-gourd
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequance_revision 30-Sep-1991 #text_change 12-Apr-1995
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C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
                                                                                                                                       10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL
                                                                                                                                                                                                                                                                                                        SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
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    2.6e-23;
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40.0%; Pred. No. 4.9e-23;
tive 46; Mismatches 53;
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                                                    Mismatches
             Pred. No.
                                               46;
    39.5%;
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A;Molecule type: protein
A;Residues: 1-247 <KON>
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Aptocession: A2670
Brand, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Brack Appl. Chem. 58, 789-738, 1986
Ariticle: Soichitific evaluation of Tian Hua Fen (THF): history, chemistry and application
A; Reference number: JT0003
A; Accession: JT00
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A;Reference number: A36274; MUID:90256790; PMID:2341400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-72, VV, 74-90, S, 92-233, Tr, 235-267, D, 269-289 «ZHE»
A,Cross-references: GB:S70176; NID:g547148; PIDN:AAB31048.1; PID:g547149
R,Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
B,D Blol. Chem. 265, 8665-8669, 1990
A,Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr
A,Reference number: A36273; MUID:90256789; PMID:2341399
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A;Reference number: A66711; PDB-TTCS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27 R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
A;Xiong, J.P.; Xia, Z.X.; Wang, Y.
A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re A;Reference number: A58622; MUID:95360714; PMID:7634073
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
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C;Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 23-Mar-2001 C;Accession: JT0566; A36274; JC1093; A36273; JT0003 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. R;Shaw, P.C.; Yung, E.J.; Ligon A;T. 1991 A;Tile: Cloning of trichosanthin cDNA and its expression in Escherichia coli. A;Reference number: JT0566; MUID:91153657; PMID:1999291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Wolecule type: DNA
A; Residues: 1-233, T', 235-246, M', 248-289 < CHO>
A; Cross-references: GB: J05434; NID: 9170534; PIDN: AAA34206.1; PID: 9170535
R; Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A; Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A; Reference number: JC1093; MUID: 94271613; PMID: 8003348
                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-289 <SHAA
A,Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A,Experimental source: tuber
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C; Keywords: abortifacient; glycosidase; hydrolase; root; toxin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-270/Product: trichosanthin alpha #status experimental <MAT>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>
F;271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;93,183,186/Active site: Tyr, Glu, Arg #status predicted
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                                                                                                                                                                                                                                                            A; Accession: JT0566
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C, Function:
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N; Contains: rRNA N-glycosidase (EC 3.2.22)
C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Date: 31-Dec 1993 #sequence revision Ol-Aug-1997 #text change 16-Jul-1999
C; Accession: S33429; JT0202; A39761; JU1398; S14472; S24133; S74110; S74111
R; Hung, C; H; Lee, M; C; Lee, T; C; Lin, J; Y.
J; Moll. Biol. 229, 269-267, 1993
A; Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor-A; Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                              N; Contrains: rNNA N-glycosidase (EC 3.2.2.2)
(Species: Abrus precatorius (Indian licorice)
(Species: Algoria (Algoria (Algoria) (Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F_j 7 - 246/Domain: rRNA N-glycosidase homology <r.v.>
F_j 7 - 246/Domain: rRNA N-glycosidase homology <r.r. Tyr, Glu, Asn) #status predicted F;164,167/Active site: Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 WAHQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNKYITVELSNSERE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 'E',2-528 <HUN>
A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A;Note: the coding region for the sequence shown is preceded by an ATG codon
A;Note: residues 1-8 were derived from the synthesized primer
B;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication, glycosidase; hydrolase; lectin; toxin
F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-251 <EVE>
R, Evenaen, G; Mathlesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A, Description: Direct molecular cloning of two distinct abrin A-chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%; Score 336.5; DB 2; Length 251; 44.9%; Pred. No. 6.8e-23; tive 24; Mismatches 69; Indels 9
                                                                                                                                                                                                                    abrin (clone 7.2) precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abrin-a precursor - Indian licorice (fragment)
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A, Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S14471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                 194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 RTRIR 194
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A; Residues: 'M', 1-251
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A;Residues: 1.289 cMIZ>
A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
B;Crodo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A;Reference number: JC5032; MUID:97108848; PMID:8951169
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N)Contains: karasurin A (Species: Trichosambes kirilowii var. japonica (Species: Josep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002 (Species: Mizukami, H.; Lida, Kr.; Kondo, T.; Ogihara, Y. Railol, Pharm. Bull. 20, 711-713, 1997 A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote A;Reference number: JC5606; MUID:97356562; PMID:9212998
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F;22-270/Product: karasurin C #status predicted <MAC>
F;24-270/Product: karasurin A #status predicted <MAC>
F;24-270/Product: rarasurin A #status predicted <MAC>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 IISVAIDVINVYVMGYRAGDISYFF---NEASAIEAAKKVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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                                                                                                                                                                                                                                                                                                                                                                                    2 VSFRLSGATSSSYGVFISNLRKALFYERKL-YDIPLL--RSTLPGSQRYALIHITNYADE
                                                                                                                                                                                                                                                                                                                                10 INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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5.9e-23;
ches 53; Indels
                                                                                                                                                                                                                                                      53; Indels
                                                                                                                                                                33.0%; Score 338; DB 2;
40.0%; Pred. No. 4.9e-23;
tive 46; Mismatches 53.
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40.0%; Pred. No. 5.9e
tive 46; Mismatches
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A;Molecule type: protein
A;Residues: 22-270 <KON>
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tes 74; Conserv
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171 IGKRV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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Gaps

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62

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Cispecies: Luffa cylindrica (smooth loofah)
Cispecies: Luffa cylindrica (smooth loofah)
Cispecies: Luffa cylindrica (revision 17-Apr-1993 #text_change 20-Aug-1999
Cistes sion: 823519; 823113
Rixacoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Rixacoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Rixacoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
A; Katecoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
A; Title: Nuclectide sequence of cpNA encoding beta-luffin, another ribosome-inactivating A; Reference number: 823519; MUID:92353400; PMID:1643290
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R;Islam, M.R.; Hirayama, H.; Funatsu, G.
Raptic. Biol. Chem. 55, 229-238, 1991
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: UN0108; MUID:91248488; PMID:1368666
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                                                                                                                     70 SVTLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFIDVQNRYTFAFGGNYDRL 127
                                                                                                                                                                                                                                           128 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 187
                                                                                                                                                                                                                                                                           C;Species: Luffa cylindrica (smooth loofah)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
                                   63 SIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD-----YLFTGT-DQHSLPFYGTYGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.0%; Score 307.5; DB 2; Length 278; 35.8%; Pred. No. 3.2e-20; tive 45; Mismatches 64; Indels 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.8 Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smooth loofah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 RTRIRYN 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                174 RVRVSIQ 180
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A, Molecule type: protein
A, Residues: 1-250 <ISL>
                                                                                                                                                                                                                                                                                                                                                                    188 EMRTRIR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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A, Residues: 1-201,203-251 <FUN>
A, Rosidues: 1-201,203-251 <FUN>
A, Rosidues: 1-201,203-251 <FUN>
A, Rosidues: 1-201,203-251 <FUN>
A, Rosidues: 1-201,203-251 <FUN>
B, St. O.: Mathiesen, A.: Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A, Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A, Reference number: A39761, MUID:91201329; PMID:2016300
A, Accession: A39761
A, Status: nucleic acid sequence not shown
A, Residues: FC, 2-251 <FVE>
A, Rosidues: BC, 2-251 <FVE>
A, Rosidues: BC, 2-251 <FVE>
A, Note: residues: 1-8 were derived from the synthesized primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikimura, M.; Sumizawa, T.; Funatsu, G.
Bisosi. Blotechnol. Blochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxio
A;Reference number: JC1398; MUID:93169023; PMID:7763422
      fra
         complete amino acid sequence of the A-chain of abrin-a, a toxic protein
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A, Molecule type: protein
A, Residues: 262-297, Y'.299-426, 'L',428-466,'P',468-482,'L',484-528 < CHE>
R, Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
R, Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
B, Lin, S.H.; Chow, L.A.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
A; Lit.e: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: 874110; MUID:97008945; PMID:8856055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: S14472
A, Accession: S14472
A, Status: preliminary
A, Molecule type: DNA
A, Estatus: ME, 2-251 (EV2)
A, Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
A, Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
A, Chen, Y. L.; Chow, L. P.; Tsugita, A.; Lin, J. Y.
FEBS Lett. 309, 115-118, 1992
A, Title: The complete primary structure of abrin-a B chain.
A, Reference number: S24133; MUID:92371656; PMID:1505674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: JC1398
A,Molecule type: protein
A;Molecule type: protein
A;Residues: 261-347'I',349-351,'A',353-357,'L',359-528 <KIM>
A;Experimental source: seed
B;Everasen, G; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
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A; Residues: 89-108;154-172 < LIN>
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         A; Title: The complete amin
A; Reference number: JT0202
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Best Local Similarity
Matches 80; Conserv
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                                                                      A; Accession: JT0202
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Search completed: February 10, 2004, 16:28:01
Job time : 11.7687 secs
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C;Species: Viscum album
C;Species: Viscum album
C;Species: Viscum album
C;Species: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C;Accession: pb0018
R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W. Biochem. Biophys. Res. Commun. 247, 377, 373, 1998
Biochem. Biophys. Res. Commun. 247, 377, 373, 1998
A;Title: Primary structure and molecular modeling of mistletce lectin I from Viscum albu A;Reference number: PD0018; MUID:98308123; PMID:9642133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agglutinin I precursor - European elder
C;Species: Sambucus nigra (European elder)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: 862627; 862619
R;Van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Bur. J. Biochem. 235, 128-137, 1996
A;Title: The Neudac(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A;Reference number: 862619; MUID:96202926; PMID:8631319
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                                                                                                                                                                                                                                                                                                                                                                                       60 AITMAIDVINVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
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                                                       Gaps
                                             11;
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                                             48; Mismatches 64; Indels
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34.2%; Pred. No. 1.2e-19;
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A.Residues: 29-39;309-319 <VA2>
C;Superfamily: ricin; rRNA N-glycosidase homology
F;37-283/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 AARFQYIEGEMRIRI 193
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200 AARFRYIELRIRTSI 214
                                                  64; Conservative
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Best Local Similarity
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A; Residues: 1-570 < VAN>
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123 GH-RDQIPLGIDQLIQSVTALRF---PGGSTRTQARSILILIQMISEAARFNPILWRYRQ 178
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                                                                                                                                                                                                                                                                   56; Indels 38; Gaps
                                                                                                                                                                                                         Length 254;
                                                                                                                                                                                                  Query Match

27.9%; Score 286; DB 2;
Best Local Similarity 38.4%; Pred. No. 2.4e-18;
Matches 81; Conservative 36; Mismatches 56;
                         A;Molecule type: protein
A;Residues: 1-254 <ESC>
C;Superfamily: ricin; rRNA N-glycosidase homology
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 YIE-------GEMRTRIRYN 196
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GenCore version 5.1.6
Copyright (c) 1993 - 2004. Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 10, 2004, 16:13:55; Search time 6.63825 Seconds (without alignments) 1409.756 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-083-336A-5 1025 1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 199

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΙD	RICI RICCO	AGGL_RICCO	ABRC_ABRPR	ABRB ABRPR	RIPT_TRIKI	RIP2_BRYDI	RIPS_TRIKI	NIGB_SAMNI		RIP1 BRYDI	RIPB LUFCY	RIP1 CUCFI	MLA VISAL	RIPA LUFCY	RIP2 MOMBA	RIP1_MOMCH	RIP1_TRIAN	RIPG_GELMU	RIPA_PHYAM	RIP1_PHYAM	RIPS PHYAM	RIPP MIRJA	RIP2_HORVU	RIP1_HORVU	RIP7_SAPOF		RIP2 PHYAM	RIP6 SAPOF	RIPO DIACA	RIP2_SAPOF	SLTA_BP933		RIP3_MAIZE
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9/0	Query	99.5	8.06	34.5	33.7	33.4	33.3	33.0	32.2	32.1	30.4	29.3	28.9	27.9	27.8	27.2	27.0	25.4	23.7	19.3	17.8	17.6	17.4	13.7	13.0	12.8	12.4	12.3	12.1	12.0	11.8	10.8	•	10.7
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RIPX_MAIZE RIP9_MAIZE	SLTA_BPH19	SLTA BPH30 SYV AQUAE	FTSH TREPA AERA AERTR	Y348_MYCPN	AERS_AERHY	AERA AERHY	RIP4_SAPOF
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107.5	91	91 85.5	85 82.5	81	78.5	78.5	92
8 8 8 4 13 6	37	დ თ ო ო	4 4 1 4	42	43	44	45

ALIGNMENTS

us-10-083-336a-5.rsp

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CONFLICT
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PDB;
PDB;
**Xin Y., Robertus J.D.;

"Analysis of several key active site residues of ricin A chain by
"Analysis of several key active site residues of ricin A chain by
"Analysis of several key active site residues of ricin A chain by

"University and X-ray crystallography.";

"In protein Eng. 5:775-779(1992).

"In protein Eng. 5:775-779(1992).

"In protein Eng. 5:775-779(1992).

"In extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 608 inbornal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28s ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell agoltutination (lectin activity). It binds to beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific adenosine on the 28S TRNA.
--- SUBDIAT: Disulfide-linked dimer of A and B chains.
--- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
--- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
--- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY: TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 galactopyranoside moieties.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-ray structure of recombinant ricin A-chain at 1.8-A resolution."; Mol. Biol. 244:410-422(1994).
                                                                         MEDLINE=87165983; PubMed=3558397;
Monfort W. Villafranca J.B., Monzingo A.F., Ernst S.R., Katzin B.,
Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Day P.J., Ernst S.R., Frankel A.B., Monzingo A.F., Pascal J.M., Molina-Svinth M.C., Robertus J.D., "Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis I., Svinth M., Day P., Monzingo A.F., Milne G.W.,
Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95082010; PubMed=7990130;
Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
Pauptit R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
MEDLINE=96374222; PubMed=8780513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDILINE=91352005; PubMed=1881882; MEDILINE=91352005; PubMed=1881882; Robertus J.D.; Robertus J.D.; Richarder of ricin B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDIINE=91352004; PubMed=1881881; Katzin B.J., Collins E.J., Robertus J.D.; Structure of ricin A-chain at 2.5 A."; Proteins 10:251-259(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
                                                          K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                          Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 35:11098-11103(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93165632; PubMed=1287657;
"Ricin.";
Toxicon 39:1723-1728(2001).
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-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
-!- CAUTION: REF.4 SADUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
-!- DATABASE: NAME=Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50231, RICIN B LECTIN; 2.
PROSITE; PS50231, SHIGA_RICIN; 1.
Plant defense; Hydrolase, Protein synthesis inhibitor; Toxin, Repeat; Glycoprotein; Signal; 3D-structure.
SIGNAL
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N-LINKED (GLCNAC. .) (IN MINOR FORM).
N-LINKED (GLCNAC. .).
N-RINKED (GLCNAC. .).
                                                                NOTE=Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .).
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RICIN B-TYPE LECTIN
RICIN B-TYPE LECTIN
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LINKER PEPTIDE
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2-BETA.
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR00174; RIP.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; I.
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                                                                                                                                                                                                                                                       EMBL, X03179; CAA26939.1; -.
EMBL, XS2908; CAA37095.1; -.
EMBL, XO2388; CAA26230.1; -.
EMBL, A12892; CAA01058.1; -.
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SMART; SM00458; RICIN; 2.
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1APG; 31-JAN-94.

1FMP; 31-OCT-93.

1IFS; 14-JAN-98.

1IFT; 14-JAN-98.

1IFU; 14-JAN-98.

1RTC; 31-OCT-93.

1OBS; 16-JUN-97.
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PDB; 11L9; 16-JAN-02
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1BR6;
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                                                                                                                                                                                                                                                             156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                           62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                 96 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 155
                                                                                                                                                                                                                                          GNYDRLEQIAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                 61
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Lin T.T.-S., Li S.S.-L.;
Lin THE N-TEMINAL SECTION;
LIN THE N-TEMINAL SECTION;
LIN THE N-TEMINAL SECTION;
LIN THEN TAMILY. TYPE 2 RIP SUBFAMILY.
-- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE=86059449; PubMed=2999130;
RODELTS L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with
                                                                                                                    36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Malpighiales, Euphorbiaceae, Ricinus.
                                                                               2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Araki T., Yoshioka Y., Funatsu G.; The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biochiya. Acta 872:277-285 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (BC 3.2.2.22); Agglutinin B chain].
Ricinus communis (Castor bean).
                                       ;
  Length 576;
                                         Indels
99.5%; Score 1020; DB 1;
100.0%; Pred. No. 2.7e-87;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                         FOYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                             216 FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M12089; AAA33869.1; -. EMBL; S40368; AAB22584.1; -.
                                             Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                        Similarity
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P06750;
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
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InterPro; IPR00172; Ricin_B_lectin.
InterPro; IPR001572; Ricin_B_lectin.
Pfam; PF00161; RIP; I.
Pfam; PF00161; RIP; I.
PROMIS; PR00458; RICIN, 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
PROSITE; PS0075; SHIGA_RICIN; 1.
PROSITE; PS0075; SHIGA_RICIN; REPEAL; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IFPKQYPIINFTTAGATVQSYINFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1993 (Rel. 41, Last annotation update)
Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)
(BC 3.2.2.22); Abrin-C B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 564;
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                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D455F2A72F609759 CRC64;
                                                                                                                                                                                                     AGGLUTININ B CAZIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
1-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .).
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N -> D (IN REF. 2).

R -> G (IN REF. 2).

R -> T (IN REF. 2).

F -> V (IN REF. 2).
                                                                                                                                                                                 AGGLUTININ A CHAIN.
LINKER PEPTIDE.
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2-ALPHA.
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Best Local Similarity 91.9%;
Matches 182; Conservative
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           HSSP; P02879; 1BR6.
GlycoSuiteDB; P06750;
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404
552
564 AA;
PIR; A24261; RLCSAG.
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P28590;
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MOOD K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;

Wood K.A., Lord J.M., Wawrzynczak E.J., Piatak M.;

"Preproabrin: genomic cloning, characterisation and the expression of the A-chain in Escherichia coli.";

Eur. J. Biochem. 198:723-732 (1991).

Eur. J. Biochem. 198:723-732 (1991).

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S TREOSOMAL SUBURITY BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE BINDING OF ABRIN TO THE CELL MEMBANE THAT PRECEDES ENDOCYTOSIS.

C. I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.

C. I. SUBUNIT: DISCLIED-LINKED DIMER OF A AND B CHAINS.

C. I. DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALbHA, BETA, GAMMA).

C. I. SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae; Abreae, Abrus.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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LINKER PEPTIDE (BY SIMILARITY).
ABRIN C B CHAIN (BY SIMILARITY).
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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                                                                                                                                                                                                                                                                                                                                                          INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains
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or send an email to license@isb-sib.ch).
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2-ALPHA.
2-BETA.
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InterPro; IPR001574; RIP. —
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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                                                                                                         MEDLINE=91266957; PubMed=2050149;
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SMART; SM00458; RICIN; 2.
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                                                                              SEQUENCE FROM N.A.
                                             NCBI_TaxID=3816;
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320
363
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198
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34.5%; Score 353.5; DB 1; Length 562;

Query Match

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                                                                                                                                                                          93 SERESIEVGIDVINAXVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                                                                                                       66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
                                                                                                                                                                                                                                                                                      149 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI 205
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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rnn.
-!- SUBUNIT: DISULFIDE-LINEED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOWAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROPEIN FAMILY. TYPE 2 RIP SUBPAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                           126 RIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFOYI
                                                              6 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EC 3.2.2.21) ADINI-D B CHAIN].
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimura M., Sumizawa T., Funatsu G.,
Kimura M., Sumizawa T., Funatsu G.,
"The complete amino acid sequences of the B-chains of abrin-a and
abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biosci. Biotechnol. Biotechnol. 57:166-169(1993).
-!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S. RRNA.
ABRIN-A IS MORE TOXIC THAN RICIN.
-!- FUNCTION: THE B CHAIN IS A GALACTORSE-SPECIFIC LECTIN THAT
PACILITARES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.; "Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABRR ABRR STANDARD; PRT; 527 AA.

000777; PR1374;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(EC 3.2.2.23); Abrin-b B chain]
                     70; Indels
45.5%; Pred. No. 2.7e-25;
                          24; Mismatches
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MEDLINE=93132798; PubMed=8421313;
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                          Conservative
                                                                                                                                                                                                                                                                                                                                           186 EGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                      206 SNRVGVSIR 214
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Best Local Similarity
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NCBI_TaxID=3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
                                                   PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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BY SIMILARITY.
PYRROLIDONE CARBOXYLIC ACID (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                               72; Indels
                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                  ABRIN-B B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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S -> N (IN REF. 2).
L -> M (IN REF. 2).
Y -> D (IN REF. 2).
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D -> N (IN REF. 2)
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      PIR; S32430; S32430.
HSSP; PILL40; ABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                     Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
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EMBL; M98345; AAA32625.1;
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324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95344383; PubMed=1619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Biochem. J. 309:285-298(1995).
-! FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Maximowicz; TISSUE=Leaf;
MEDLINE=90256790; PubMed=2341400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                       01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor
(rRNA N-glycosidase) (EC 3.2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliaphyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Maximowicz; TISSUB=Tuberous root;
MEDLINE=90256789; PubMed=2341339;
Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
Wu P., Hwang K., Piatak M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                       STRAIN-Maximowicz;
MBDINIR-21155677; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
Proteins 19:4-13(1994).
    289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94344957; PubMed=8066085;
                                        01-MAR-1989 (Rel. 10, Created)
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             Gene 97:267-272(1991).
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PDB; 1MRJ; 07-FEB-95.

PDB; 1MRK; 07-FEB-95.

PDB; 1J4G; 28-JAN-03.

PDB; 1J4G; 28-JAN-03.

PDB; 1J5 21-JAN-03.

PDB; 1J0D2; 24-ARR-00.

InterPro; IPR001574; RIP.

PRIM: PF00161; RIP; 1.

PROSITE; PS00275; SHIGARICIN.

PROSITE; PS00275; SHIGARICIN.

PROSITE; PS00275; Antivital; Protein synthesis inhibitor; Hydrolase;
                                                                            RIBOSOME-INACTIVATING PROTEIN ALPHA-
                                                                                            | FPL -> LEPLI (IN REF. 4).
| MISSING (IN REF. 4).
| -> L (IN REF. 4).
| V -> VDAGLERNAVL (IN REF. 4).
| KI -> GL (IN REF. 4).
| K -> S (IN REF. 4).
| WS -> LWL (IN REF. 4).
| WS -> LWL (IN REF. 4).
| WS -> T (IN REF. 4).
| WS -> T (IN REF. 5).
| MISSING (IN REF. 2).
| MISSING (IN REF. 2).
                                                                                 TRICHOSANTHIN.
MISSING IN MATURE PROTEIN
BY SIMILARITY.
 or send an email to license@isb-sib.ch).
                                                                    Toxin; Signal; 3D-structure.
         EMBL; M34858; AAA34207.1; -. EMBL; J05434; AAA34206.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                          129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
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                                                                                                                                                                                                                                                                                                                                81
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Bioconj. Chem. 5:423-429(1994).

-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

-!- CARALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                         33.4%; Score 342; DB 1; Length 289;
39.5%; Pred. No. 1.4e-24;
tive 46; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIPZ BRYDI STANDARD; PRT; 282 AA.
P98184; Q9SBJO;
16-COT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.2) (BD2).
Bryonia dioica (Red bryony).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siegall C.B., Gawlak S.L., Marquardt H.;
"Bryodin 2 a ribosome-inactivating protein isolated from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff B.A., Mixan B.,
Marquardt H.;
                                                                                      31676 MW; SCE09BB630575BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bryonia dioica.";
Patent number US5597569, 28-JAN-1997.
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HSSP; P09989; 1MRJ.
                                                                                                                                                                         Local Similarity 39.58
260 2
263 2
266 2
289 AA;
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                                                                                                                                                                                                                                                                                                                                    69 LSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                    81 ESVTVALDVVNVXVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLE 136
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                                                                                                                                                                                                                                                                                                                                                                                                        129 QLAGNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Root tuber;
MEDLINE=97356562; PubMed=9212998;
Mizukami H., Tida K., Kondo T., Ogihara Y.;
"Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60S RIBOSOMAL SUBENNITS.

CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                   INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPN-RVGLPINQRFILVELSNHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                               RIBOSOME-INACTIVATING PROTEIN BRYODIN II
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                              13;
                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
C52BE2F6A873769C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE OF 24-270.
MEDLINE-92005921; PubMed=1914000;
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,
Pfam; PF00161; RIP; I.
PRINTS; PR00396; RICARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Multigene family; Glycoprotein; Signal.
21
21
                                                                                                                                                                                                DB 1; Length 282;
                                                                                                                                                                                                                                  57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR.1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3-2.2.2).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                  33.3%; Score 341.5; DB 1
48.0%; Pred. No. 1.5e-24;
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                                                                                                                                BY SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kirilowii var. japonica.";
Biol. Pharm. Bull. 20:711-713(1997)
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                                                                                                             22 282 RI
183 183 BY
25 25 N-
282 AA, 30754 MW;
                                                                                                                                                                                                                                  86; Conservative
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P24478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
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Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
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01-007-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nigtin b precursor (Agglutinin V) (SNAV) (Contains: Nigrin b A chain
CRNA N-Glycosidase) (EC 3.2.2.22); Nigrin b B chain].
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                              Length 289;
                                                                                                                                                                                                                                                                                                                                                                                         53; Indels
                                                                                                                                                                                                                                                                                   183 183 BY SIMILARITY.
289 AA; 31704 MW; 883D3E3242887B26 CRC64;
                                                                                                                                                                                                                                          KARASURIN-A.
REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                                                33.0%; Score 338; DB 1; 40.0%; Pred. No. 3.3e-24;
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EMBL; AB000666; BAA21786.1;
                                                      HSSP; P09989; 1MRJ.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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270
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289
                 PIR; JC5606; JC5606.
PIR; JU0393; JU0393.
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Matches 74; Conserv
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142 DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY 194
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=93132798; PubMed=8421313;
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                                                                                                                                            STANDARD;
                                185 IEGEMRTRIR 194
                                                             195 İEQEVRRSLQ 204
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                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3816;
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
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 PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM FOSITION 4,324 OF 28 S RNA. THE B CTAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                                             -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN PAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
SIGNAL
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F250CBE24621BF14 CRC64;
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NIGRIN B B CHAIN.
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N-LINKED
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InterPro; IRR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP_Fem, PF00165; Ricin_B_lectin; 6.
Fam, PF00165; Ricin_B_lectin; 6.
PRINTS; PR00156; RICAL
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                     entities requires a license agreement
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1-GAMMA.
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563 AA;
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les 75; Conserv
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-!- SUBULIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAWAA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
P11140: P28589;
01-UUL-1989 (Rel. 11, Created)
01-UUL-1989 (Rel. 2), Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2013 (Rel. 41, Last annotation update)
Abrin-a precursor (Contains: Abrin-a A chain (rRNA N-glycosidase)
(BC 3.2.2.22); Abrin-a B chain)
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic
protein from the seeds of Abrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **LSAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
**MEDLINE=9533188; PubMed=760896;
Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
"Crystal structure of abrin-a at 2.14 A.";
J. Mol. Biol. 250:354-367(1995).
-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALITIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNAA.
ABRIN-A IS MORE TOXIC THAN RICIN.
-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                             Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y., spring structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.", J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
"The complete primary structure of abrin-a B chain.";
PESS Lett. 309:115-118(1992).
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us-10-083-336a-5.rsp

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70 SVTLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 127
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Matches 80; Conserv
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                                                                         EMBL; M98344; AAA32624.1; ALT INIT.

REMBL; M54872; -; NOT ANNOTATED CDS.

PIR; 532429; TZLSA.

PIR; 532429; TZLSA.

REMBL; AS4800772; Ricin B lectin.

REPDB; 1ABR; 07-FEB-95.

RICEPTO; IPRO0172; RICin B lectin; 6.

Pfam; PP00652; RICin B lectin; 6.

Pfam; PP00652; RICin B lectin; 6.

RART; SM00489; RICIN; 2.

RART; SM00489; RICIN; 2.

ROSITE; PS00273; RICIN; 1.

PROSITE; PS00275; SHIGARICIN; 1.

ROSITE; PS00275; SHIGARICIN; 1.

ROSITE; PS00275; SHIGARICIN; 1.

ROSITE; PS00275; SHIGARICIN; 1.

ROSITE; PS00275; RICIN; 1.

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PROPAIN 273 400 RICIN B-TYPE LECTIN 2.

REPEAT 328 366 1-BETA.

REPEAT 369 401 1-GAMMA.

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ROBERT 4449 2-ALPHA.
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MISSING (ILN REF. 2).
N -> Y (IN REF. 4).
M -> L (IN REF. 4).
T -> P (IN REF. 4).
T -> P (IN REF. 4).
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INTERCHAIN (BY SIMILARITY).
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-I. FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS

-I. FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS

-I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-I. PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PRODUCE A SHORTER PROTEIN.
                                                                                                                                                                                                                                                                P31385; Q9S819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(RC 3.2.2.22) (BD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                           Bryonia dioica (Red bryony).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
Suromatobi, Cucurbitales, Cucurbitaceae, Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOTECHNOLOGY: Especially useful as immunctoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97228081; PubMed=9115985;
Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.
Siegall C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'N-terminal sequence of some ribosome-inactivating proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent number US5541110, 30-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89326691; PubMed=2753596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Root;
MEDLINE=95151812; PubMed=7849072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 36:3095-3103(1997).
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                           188 EMRTRIR 194
                                                                                                                                                           174 RVRVSIQ 180
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TYPE 1 RIP SUBFAMILY.

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             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 EMBL outstation
                                                                                                                                                                                                                                                                       RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL)
E-K: REDUCES ACTIVITY: 10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                                                                                                                                                         Prim. PROGETS RIP, 1. P. P. PRIM. PROGETS RICARION. PROSITE; PRO036; SHIGARICIN. PROSITE; PS00275; SHIGARICIN. 1. Plant defense; Protein synchesis inhibitor; Hydrolase; Toxin; 3D-structure; Multigene family; Glycoprotein; Signal. 23 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.4%; Score 312; DB 1; Length 290 37.3%; Pred. No. 8.6e-22; Live 46; Mismatches 58; Indels
the Swiss Institute of Bioinformatics and the
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                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                          EMBL; I24020; -; NOT_ANNOTATED_CDS.
PRF; S16491; S16491.
PDB; 1BRY; 04-WAR-98.
InterPro; IPR001574; RIP.
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RESULT 13
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                                                70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AITWAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                              70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-:- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
S SFRISGATITSYGVFIKNIREALPYERKV-YNIPLL--RSSISGSGRYTLLHITNYADE
                                                                                                                                                                                                                                                                                         (EC 3.2.2.2).

Luffa cylindrica (Smooth loofah) (Sponge gourd).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Islam M.R., Hirayama H., Funatsu G.; "Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds."; Agric. Biol. Chem. 55:229-238(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 300.5; DB 1; Length 250; 34.2%; Pred. No. 8.4e-21;
                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA; 27293 MW; F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91248488; PubMed=136866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JN0108; JN0108.
HSSP; P16094; 1AHC.
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                                                                                                                                 189 MRTRI 193
                                                                                                                                                        194 IGKRV 198
                                                                                                                                                                                                                   RIPB LUFCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 NTITMAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL-PNRVGLPINQRFILVELSNHAE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Biotechnol. 17:337-340 (2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRRA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1; Cucurbitales, Cucurbitaceae, Cucumis.
NCBI_TaxID=131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00161; RIP; 1.
RNIVIS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 296.5; DB 1; Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada T., Ohki S.T., Osaki T.;
"Cloning and analysis of a cDNA coding a putative ribosome-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 POTENTIAL.
286 PUTATIVE RIDOSOME-INACTIVA
1185 N-LINKED (GLCNAC. .) (PO
110 N-LINKED (GLCNAC. .) (PO
252 N-LINKED (GLCNAC. .) (PO
31771 MW; 4EFD4966E604DA41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 2.3e-20; 47; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inactivating protein from Cucumis figarei.";
                             286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB045560; BAB19677.1; -. HSSP; P16094; IAHC.
InterPro; IPR001574; RIP.
                                                                                  16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.4%;
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                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 MRTRIRYNR 197
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196 IIDRISVSK 204
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252 2
286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Cucumis figarei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toxin; Signal.
                             CUCFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                     Q9FRX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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CUCFI
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"Complete amino acid sequence of the A chain of mistletoe lectin I.";
FBBS Lett. 399:153-157(1996).
                                                                                                                                                                                                                                                                                                                                                  AND NON-GIYCOSYLATED FORM MLA'.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA
                                                                        Eukaryota; Viridiplantae.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.
                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2013 (Rel. 41, Last annotation update)
glycosidase) (G. 3.2.2.22).
Viscum album (Buropean mistletoe).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase, Toxin, Repeat, Glycoprotein, Lectin.
165 BY SIMILARITY.
                                                                                                                                                     MEDLINE=97134581; PubMed=8980141;
Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 286; DB 1; Length 254; 38.4%; Pred. No. 1.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53BAF98D3E0FFE67 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> A (IN MLA').

-> D (IN MLA').

A -> B (IN MLA').

-> M (IN MLA').

-> F (IN MLA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P -> 1 (IN MA)
T -> S (IN MA)
Y (IN MA)
MAA'
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T -> S (IN MLA')
D -> S (IN MLA')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N -> T (IN MLA')
P -> T (IN MLA')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E -> D (IN MLA')
 254 AA.
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 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICI
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001574; RIP.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 PIR; PD0018; PD0018.
                                                                                                                                           STRAIN-Subsp. album;
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 AA;
                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P11140; 1ABR.
                                                                                                          NCBI_TaxID=3972;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query ...
Best Local Similar
 VISAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITE
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-:- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 VRFSLSGSSSTSYSKFIGDLRKALPSNGTVYNITLLLSSASGA---SRYTLMTLSNYDGK
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                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.22).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIBOSOME-INACTIVATING PROTEIN LUFFIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92288316; PubMed=1600156; Kataoka J., Habuka N., Miyano M., Maeuta C., Koiwai A.; Kataoka J., Habuka N., Miyano M., Maeuta G., Koiwai A.; Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica."; Plant Mol. Biol. 18:1199-1202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 284.5; DB 1; Length 277;
132 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EA17FC27998C25AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.9e-19;
                                                                                                      179 YINSGASFLPDVYMLELETSWGQQSTQVQHS 209
                                                                       ----GEMRTRIRYN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 B
30212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X62371; CAA44229.1; -. PIR; S22494; S22494.
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InterPro; 1PR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Conservative
                                                                                                                                                                                              STANDARD;
                                                                 184 YIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
20
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                                                                                                                                                                                              LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE
SEQUENCE
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10;

56; Indels

36; Mismatches

Conservative

Similarity

72 TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 131

14 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 71

9 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQQQDSV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 TISVAIDVTNVYVAYRTRDVSYFF---KESPPEAYNILFKGTR-KITLPYTGNYENLQT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                   130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 INFITAGATVQSYTNFIRAVRGRLITGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ortigao M., Better M.;
"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologome to other plant proteins.";
Nucleic Acids Res. 20.4662-4662[1992].
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELOONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-Jycosidase) (EC 3.2.2.2.)
18-Jycosidase) (EC 3.2.2.2.2)
18-Jycosidase) (EC 3.2.2.2.2)
18-Jycosidase) (Bitter gourd) (Balsam pear)
18-Jycosidase) (Bitter gourd) (Balsam pear)
18-Jycosidase)
18-Jycosidase)
18-Jycosidase, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
18-Jycosidas 1; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z12175; CAA78166.1; -.
PIR; S25560; S25560.
PDB; 1CF5; 07.5UN-9.
INCEPPO; IPRO01574; RIP.
PFam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSTE; P800255; SHIGARICIN.
PROSTE; P800275; SHIGARICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.2%; Score 279; DB 1; Length 286;
35.3%; Pred. No. 9.9e-19;
tive 42; Mismatches 67; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II.
181 181 BY SIMILARITY.
286 AA; 32031 MW; 3BB9FFIAEGB25986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93027170; PubMed=1408771;
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                                                                                                                                                                                                                       STANDARD;
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                                                                                                                     191 IERISKNO 198
                                                                               190 RTRIRYNR 197
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P29339;
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Db 138 AAHKIRENIDLGLPALSSAITTLFYYNA----QSAPSALLVLIQTTAEAARFKYIERHV 192
QY 190 RTRIRYN 196
Db 193 AKYVATN 199
Search completed: February 10, 2004, 16:23:23
Job time: 7.63825 secs
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February 10, 2004, 16:17:00; Search time 26:553 Seconds (without alignments) 1933.961 Million cell updates/sec
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1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 199
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        - protein search, using sw model
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sp_virus:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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Maximum DB seq length: 200000000
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2: sp_bacteria:*
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Perfect score:
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                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q41174 ricinus com	Q94bw3 cinnamomum	Q94bw4 cinnamomum	Q94bw5 cinnamomum	Q9fv22 cinnamomum	004367 sambucus ni	Q9avr2 sambucus eb	Q06076 abrus preca	Q94ke4 trichosanth	Q9lre3 trichosanth	Q41216 trichosanth	Q38760 abrus preca	Q945s2 sambucus ni	Q8gt32 sambucus ni	Q38761 abrus preca	Q8lpv7 trichosanth
COLUMNIA	D	041174	Q94BW3	Q94BW4	Q94BW5	Q9FV22	004367	Q9AVR2	00000	Q94KE4	Q9LRE3	041216	038760	094582	Q8GT32	038761	Q8LPV7
	DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	% Duery Match Length DB	541	580	580	581	549	563	564	528	289	247	289	252	563	563	252	270
	* Query Match	99.2	39.5	38.8	38.8	38.6	34.2	33.9	33.6	33.2	33.0	33.0	32.8	32.2	32.2	32.1	31.6
	Score	1017	401.5	397.5	397.5	395.5	350.5	347.5	344.5	340	338	338	336.5	330.5	330.5	329.5	324
	Result No.		2	e	4	Ŋ	9	7	00	6	10	11	12	13	14	15	16

	Q41257 momordica c 004358 iris hollan Q8w2e7 iris hollan 004356 iris hollan Q9m633 polygonatum Q8gzn9 euphorbia s Q8vyu0 jatropha cu Q8w2e8 iris hollan
Q96236 Q96237 Q96237 Q96215 Q96215 Q96235 Q96629 Q96629 Q91358 Q81358 Q81358 Q81358 Q81358 Q81358 Q81358 Q81358 Q81435 Q81245 Q81245 Q81245 Q81245 Q81247 Q8124 Q81247 Q81	Q41257 Q04358 Q04358 Q04356 Q9M653 Q8GZN9 Q8WZE8
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 148
                                                                                                          121
                                                                                                                                                               181
                                                                                                                                                                                       121 GNYDRLEOLAGNIRENIELGNGPLEERISALYYSTGGTOLPTIARSFIICIOMISEAAR 180
                                                                                                                                  61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039803; AAK82460.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y.; Yang O., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLEQLAGNLRENI ELGNGPLEEAI SALYYSTGGTQLPTLARSFII CIQMISEAARFQYI
                                                                                                          ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                     1 IFPRQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLFINQRFILV
                                                                                                                                                              GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
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                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
NCBI_TaxID=13429,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN 111.
580 AA; 64421 MW; 940D10F01E7FB558 CRC64;
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99.2%; Score 1017; DB 10; Length 541;
99.5%; Pred. No. 1.9e-87;
iive 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.2%; Score 401.5; DB 10; Length 50.0%; Pred. No. 2.8e-29; tive 28; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PSS0231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                             181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                     FOYIEGEMRIRIRYNRRS 199
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                           Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
 Query Match
Best Local Similarity
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66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patterns.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 YPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSN-
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-!- SIMILARITY: BELCHGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AV039802; AAK82459.1; --
INTERPO: IPR000772; Ricin_B_lectin.
INTERPO: IRR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00651; Ricin_B_lectin; 6.
                                                                                                                                                                                                                                                                                                                                                              Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase). Cinnamomum camphora (Campbor tree). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang Q., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating progenes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.8%; Score 397.5; DB 10; Length 580; 49.5%; Pred. No. 6.7e-29;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).
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37E4289ECCE0CBFF CRC64;
                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SMART; SM00458; RICIN, 2.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Hydrolase; Signal; Toxin.
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                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 EYRVRESI 214
186 EGEMRTRI 193
                                                          207 EYRVRESI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Yang Q., Gong Z.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=13429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFOYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 YQTVTFTTKNATKTSYTQFIEALRAQLASGES-PHGIPVMRERSTVPDSKRFILVELSNW 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie L., Liu W.-Y., Wang E.-D.;
"Molecular cloning of cinnamomin A-, B-chain and the expression,
purification, characterization and mutagenesis of the A-Chain.";
purification, characterization and mutagenesis of the A-Chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AP255948; AAF68978.2; -.
HSSP; P02879; 2AAI.
                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                   "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 38.8%; Score 397.5; DB 10; Length 581;
l Similarity 50.0%; Pred. No. 6.7e-29;
94; Conservative 27; Mismatches 60; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9FV22;
01-MXR-2001 (TrEMBLrel. 16, Created)
01-MXR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.2) (rRNA
                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039801; AAK82458.1; -.
InterPro; IPR000772; Ricin_Blectin.
InterPro; IPR000574; Ricin_Blectin.
Pfam; PF00652; Ricin_Blectin; 5.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS50231; RICIN, 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-glycosidase) (Fragment).
Camplor (Zamplor tree).
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
Cinnamomum camphora (Camphor tree).
Makaryota, Viridiplantee; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum. NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CINNAMOMIN I.
6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                          SEQUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581 AA; 64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 EGEMRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 EYRVRGSI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=13429;
                                                                                                                                                                              patterns.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AADSPVTLAVDVINAYVVAYRTGSQSFFLREDNP--PAIENLLPDTK-RYTFPFSGSYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 DLEGVAGERREEILLGMDFLENAISALWISNL--NQORALARSLIVVIQWVAEAVRFRFI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 RLEQLAGNIRENIBLGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant J. 12, 225-1266 (1997).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARMY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; U76524, AAC15886.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIBOSOME INACTIVATING PROTEIN, A CHAIN. S63 RIBOSOME INACTIVATING PROTEIN, B CHAIN. 62336 MW; 3ED2B6CO8E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                       38.6%; Score 395.5; DB 10; Length 549; 50.0%; Pred. No. 9.5e-29; tive 27; Mismatches 60; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UUL-1997 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
Peumans W.J.:
                                                                                                                                                                                                                                                     1 1
549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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InterPro; IPR001574; RIP.
Pfam; PF0052; Ricin B_lectin; 6.
Pfam; PF00161; RIP; 1.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                        PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98112023; PubMed=9450339;
                                                               Pfam; PF00652; Ricin B lectin; 5. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sambucus nigra (European elder).
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SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                 94; Conservative
                                         InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Signal; Toxin.
SIGNAL 1 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 EYRVRGSI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 5
563 AA;
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                     Hydrolase; Toxin.
                                                                                                                                                                                                                                           NON TER
SEQUENCE
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SEQUENCE
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      RESERVED SERVED 
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142 DNLETAAGTRRESIELGPNPLDGAITSLWY--DGG----VARSLLVLIQWVPEAARFRY 194
DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q94KE4;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
SMRIYE; PR00396; SHIGARICIN.
SWART; SM00458; RICIN; 2.
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                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS50231; RICIN B LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M98346; AAA32626.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                         185 IEGEMRTRIR 194
                                                                                                                   || |:| ::
195 IEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNRVGVSIR 180
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528 AA;
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SEQUENCE
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    125
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Best Local
                                                                                                                                                                                                                                                                        206076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                             99
                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.; "Molecular cloning of ebulin 1."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-: CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                                                                                           7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                                                                                                                                    28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
                                                                                                                                                                                    67 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI --THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Gaps
                                                15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFIC ADENOSINE ON THE 288 RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AJ400822; CAC33178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sambucus ebulus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campamalids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 564;
    DB 10; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.9%; Score 347.5; DB 10; Length 5
41.1%; Pred. No. 3.4e-24;
tive 41; Mismatches 56; Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
8261681A6DB55CB8 CRC64;
    Query Match 34.2%; Score 350.5; DB 10; Best Local Similarity 41.6%; Pred. No. 1.8e-24; Matches 79; Conservative 40; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50231; RICÍN B LECTIN; 2.
PROSITE; PS00275; SHIGA-RĪCIN; 1.
Glycosidase; Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02879; 2AAI.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin B_lectin; 6.
Pfam; PF00161; RIP; I_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 564 E
564 AA; 62694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         185 IEGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                  IEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 SERESIEVGIDVTNAYVVAYRAGGQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93132798; PubMed=8421313; MEDLINE=93132798; PubMed=8421313; MEDLINE=93132798; PubMed=8421313; MEDLINE=93132798; PubMed=841... i.in J.-Y.; Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.; Primary structure of three distinct isoabrins determined by cDNA sequencing: conservation and significance."; J. Mol. Biol. 229:263-267(1993).

-! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.

-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVBLSN
                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2.2) (rRMA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye)
Eukaryota; Viridiplantae; Streptophyta; Bukryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.6%; Score 344.5; DB 10; Length 528; 45.0%; Pred. No. 5.9e-24; Live 24; Mismatches 71; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58870 MW; 62ED42FB8FFE60F8 CRC64;
528 AA
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us-10-083-336a-5.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/GenBank/DDB1 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                             Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL, AB039324; BAA92530.1; -. HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                    SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF367252; AAK52960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last amnotation update)
Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
                  11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
richosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            1 23 POTENTIAL.
24 270 TRICHOSANTHIN.
289 AA; 31706 MW; A6D5602549CAS657 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.2%; Score 340; DB 10; 39.5%; Pred. No. 6.8e-24;
                                                                           Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trichosanthes sp. Bac Kan 8-98.
Eukaryota; Viridiplantae; Streg
                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00161; RIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |:
194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=118182;
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                      NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9LRE3
Q9LRE3;
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                                                                                                                                                                                                                                                           59 IISVAIDVTNVVVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                    129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                     70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 IISVAIDVISVYIMGYRAGDISYFF---NEASAIEAAKYVFKDAMRKVTLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1; Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                               2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALVHLTNYADE
                                                                                                                                                                               10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Indels 12; Gaps
                                                                                                                   33.0%; Score 338; DB 10; Length 247;
40.0%; Pred. No. 8.5e-24;
tive 46; Mismatches 53; Indels 12;
                                                                                   247 AA; 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q41216;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC. 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.0%; Score 338; DB 10; Best Local Similarity 39.5%; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGURE PRODUCT TO PROPERTY BIP.

PERMY PRODICT, RIP. 1.

PRINTS; PROD396; SHIGARICIN.

PROSITE; PSO0275; SHIGA_RICIN; 1.
              PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S70176; AAB31048.1; -.
HSSP; P09989; 1MRJ.
                                                                                                                                                 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                          247
Pfam; PF00161; RIP; 1
                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                              189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                              171 IGKRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Toxin.
SEQUENCE 289 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3677;
                                                                        247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRICHOSANTHIN,
                                                        NON TER
NON TER
SEQUENCE
                                                                                                                    Query Match
                                                                                                                                      sest Local
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177 GVSIR 181
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Q945S2
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       129 OLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                             6 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNRYITVELSNSRRE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SRNA. ARRINATE IS CATELY THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACYDE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91201329; PubMed=2016300;
Evensen G., Mathiesen A., Sundan A.;
"Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; Repeat, Glycoprotein; Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                  252 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001574; RIP.
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                                                                                                                                                189 MRTRI 193
                                                                                                                                                                                                                    194 IGKRV 198
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                                                                                                                                                                                                                                                                                                                              RESULT 12
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67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 YPSVSFNLDGAKSATYRDFLSNLRRTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
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EMBL; AF409135; AAL04123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin 1 precursor
(EC 3.2.2.2.22).
Sambucus nigra (European elder).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                            Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Damme E.J.M.; "Characterization and cloning of lectins and ribosome-inactivating proteins from Sambucus nigra leaves.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.2%; Score 330.5; DB 10; Length 563; 39.5%; Pred. No. 1.4e-22; ive 39; Mismatches 61; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Toxin.
SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein (EC 3.2.2.2) (rRNA
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   563 AA
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InterPro; IPR001574; Ricin B lectin.
Fram, PR00652; Ricin B lectin; 6.
Pfam; PR00161; Rip; I.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00218; RICIN; 2.
PROSITE; PS00215; SHIGARICIN; 1.
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PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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124
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                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                         28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVIRRESEVQVKSRFVLVPLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Biochem. 219:83-87(1994).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                   Girbes T., Arias F.J., Antolin P.;
"Characterization and molecular cloning of Nigrin 1, a type two
"Characterization protein from leaves of elder (Sambucus nigra).";
ribosome-inactivating protein from leaves of elder (Sambucus nigra).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF249280; AAN86130.1; -.
                                                                                                                                                                                                                                                                                                                                                     7 YPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI - THLFIDVQNRYIFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae, Papliionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                               15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.; "Cloning and expression of three abrin A-chains and their mutants
                                                                                                                                                                                                                                                                       ch 32.2%; Score 330.5; DB 10; Length 563; I Similarity 39.5%; Pred. No. 1.4e-22; 75; Conservative 39; Mismatches 61; Indels 15;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ricin A-chain type 73 (EC 3.2.2.22) (FRNA N-glycosidase)
                                                                                                                                                                                                                   Hydrolase, Glycosidase.
SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94139756; PubMed=8307038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X54873; CAA38655.1; -. EMBL; X76720; CAA54138.1; -. HSSP; P11140; IABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2-252 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 IEGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 İEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        038761; 096234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Seed;
                                                                                                           rissum=reaf;
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70 SVTLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 127
                                                                                                                                                                                                                                   64 SIEVGIDVTNAYVVAYRAĞTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYĞDL 117
                                                                                                                                                                                                                                                                                                          128 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 187
                                                                                                                                                                6 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE 63
                                                                                                                                       10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                       13; Gaps
                                                                    DB 10; Length 252;
                                                                                                       66; Indels
                 252 252
252 AA; 28229 MW; 187BBB4E134AECE5 CRC64;
                                                                 32.1%; Score 329.5; DB 10
ilarity 42.8%; Pred. No. 5.5e-23;
Conservative 28; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       completed: February 10, 2004, 16:26:37
me : 29.553 secs
Glycosidase; Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                               188 EMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                                  175 RVRVSIQ 181
                                                                                Local Similarity
nes 80; Conserv
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SEQUENCE
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Job time :
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February 10, 2004, 16:13:20 ; Search time 32.2239 Seconds (without alignments) 930.966 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseqy-embl/AA1983.DAT:*
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| SIDSI/gcgdata/geneseqy-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:*
| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIFPKQYPIINFTTAGATVQ........ARFQYIEGEMRTRIRYNRRS 189
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                  OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ricin A chain. Un	Ricin A-chain (RTA	Ricin A-chain ribo	Ricin A-chain RIP.	Ricin A. Escheric	Sequence of Ricinu	Ricin A encoded by	Anti-cataract immu	Ricin D. Ricinus
SUMMARIES	ID	AAR37290	AAR63902	AAW25136	AAW21699	AAP70097	AAP70838	AAP95639	AAR70827	AAP90079
	DB	14	16	18	18	00	œ	10	16	10
	e Match Length DB	267	267	290	290	332	332	332	554	562
ۇ غ مە	Match	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9
	Score	951	951	951	951	951	951	951	951	951
, i	No.		7	e	4	S	9	7	80	σ

565 6 AZ 576 22 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Sequence of prepro	Castor bean prepro	Modified castor be	Sequence of Ricinu	Castorbean ricin.	Castor bean ricin	Ricinus communis r	Castor bean prepro				u u	Preproricin. Rici	Sequence of Ricinu	DNA sequence of ri	Ricin A from pICI1	Amino acid sequenc	Ricin A gene produ	Ricin A chain (RTA	Ricin A. Syntheti	Castor oil plant a	R. communis agglut	Sequence of Ricin	Ricin agglutinin A	Trichosanthin anti	Amino acid sequenc	Synthetic alpha-tr		ٽ	Trichosanthin. Tr	Trichosanthin from	Trichosanthin from	Trichosanthin prot	Encodes chinese cu	Alpha-trichosanthi	Chinese cucumber a
951 97.9 565 951 97.9 565 951 97.9 565 951 97.9 565 951 97.9 576 951 97.9 576 951 97.9 576 951 97.9 576 940 97.9 576 940 97.9 576 940 97.9 576 940 97.9 576 940 97.9 576 940 97.7 576 941 96.9 576 941 97.9 576 942 97.7 578 944 97.2 574 941 96.9 574 941 96.9 574 942 97.0 574 941 96.9 567 942 97.0 574 944 97.0 574 944 97.0 574 947 97.0 574 948 97.0 576 978 978 978 978 978 978 978 978 978 978	AAP50166	2 AAG78300	~		6	0		7			ď	4		4	0	m	AAB1926						Æ			_		·	AAW2514						15 AAR55129	18 AAW10468
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	97.9	7	97.9	97.9	97.9	97.9	97.9	97.9	97.9	7.76	97.5	97.4	97.4	97.2	97.0	6.96	6.96	8.96	96.2	94.5	88.7	88.7	82.5	73.9	34.6	34.6	34.6	34.6	34.6	34.6	34.6	34.6	•	4.	4.	34.6
	951	951															941	940	934	918	861.5	861.5	801.5	718	336	336	336	336	336	336	336	336	336	336	336	336
	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27				31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
                                                                                                                                                                                                                                           Lei SP;
                                                                                                                                                                                                                                           Carroll SF, Lane JA,
                AAR37290 standard; protein; 267 AA.
                                                                                                                                                                                92WO-US09487.
                                                                                                                                                                                                91US-0787567.
92US-0901707.
                                                 (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                           Berhard SL, Better MD,
                                                                                                                                                                                                                                                           WPI; 1993-167617/20.
                                                                                                                                                                                                                          (XOMA ) XOMA CORP.
                                                                                   Ricin A chain.
                                                                                                                             Unidentified.
                                                                                                                                              WO9309130-A1.
                                                                                                                                                                                 04-NOV-1992;
                                                                                                                                                                                                 04-NOV-1991;
                                                25-MAR-2003
09-JAN-2003
13-SEP-1993
                                                                                                                                                                                                         19-JUN-1992;
                                                                                                                                                                13-MAY-1993.
                                AAR37290;
RESULT 1
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. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                      1 IPPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                       The invention covers analogues of Type I RIPs. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment.

(Updated on 09-JNM-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                         --VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                            10; Gaps
                 cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) encoding type I ribosome-inactivating proteins
Analogues of type I ribosome inactivating protein - useful as
                                                                                                                                                                                                                                                                                                                          97.9%; Score 951; DB 14; Length 267; 94.9%; Pred. No. 1.3e-93; tive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carroll SF;
                                                                                                                                                                                                                                                                                                                                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Studnicka GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR63902 standard; protein; 267 AA
                                                                Claim 1; Page 92; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0064691
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                         Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carroll SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-006804/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin A-chain (RTA)
                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                           267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9426910-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-NOV-1994.
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR63902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                     52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                     ---VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                       Which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                                                                              gene product, it is analogous to the (RIPs) described in AAR63903-R63911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin A-chain ribosome inhibitory protein inactive precursor.
                                                                                                                                                                                                                                                                                                         Length 267;
                                                                                                                                                                                                                                                                                                                                        0; Indels
which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                                                                        Score 951; DB 16;
Pred. No. 1.3e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW25136 standard; Protein; 290 AA.
                                            Example 3; Fig 1; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FOYIEGEMRTRIRYNRRS 198
                                                                            AAR63902 is the ricin A chain g
ribosome-inactivating proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0485286.
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                                                                                                                                                                                                                                                                                                         97.98;
                                                                                                                                                                                                                                                                                                                       94.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                        Matches 188; Conservative
                  therapeutic agents.
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                           267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS5646026-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1997
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW25136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
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                                                                                                                                                                                                                                                                                                         Query Match
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(DOWC) DOWELANCO.

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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins possible invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidaes activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proteins make it possible to provide protein possible. The RIP can be used to make cytotoxic conjugates.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 10; Gaps
/note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Inactive precursor of maize ribosome-inactivating protein - e
chimeric ribosome-inactivating protein precursors containing
internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.9%; Score 951; DB 18; Length 290; 94.9%; Pred. No. 1.4e-93; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Column 91-94; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                             Walsh TA;
                                                                                                                                                                                                                             90US-0535636.
95US-0378761.
                                                                                                                                                                                                          92US-0987927.
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Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                             Hey TD, Morgan AER,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-309831/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 290 AA;
                                                                                                                                                                                                                                                                                                (DOWC ) DOWELANCO.
                                                                                                                                                               26-JAN-1995;
                                                                                                                                                                                                                                11-JUN-1990;
26-JAN-1995;
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                                                                         US5635384-A
                                                                                                                  03-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
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       EX HX SX
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                                                                                                                                                                                                                                            AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and beta units of the RIP. When
separated the two units regain and beta units of the RIP. When
separated the two units regain and beta units of inactivating
cukaryotic ribosomes and hence preventing protein production. Many
different RIPs may be produced with an internal linker including
maize RIP. Trichosanthin, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as tumour cells via the
ttachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see US4869903). There is interest
the capacity to provide correct post-translational processing. However,
RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
in cell death. Since the inactive RIP proteins are not cyctoxic to
cukaryotic cells, they can be recombinantly expressed in such cells and
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; linactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                             DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 951; DB 18; Length 290; 94.9%; Pred. No. 1.4e-93; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----
                                                                                                                                                                                                   Claim 4; Column 91-94; 186pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW21699 standard; Protein; 290 AA
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                            Walsh TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188; Conservative
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                                                                     WPI; 1997-362934/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ricinus communis.
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26-SEP-1997
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Best Local S
                            Hey TD,
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Matches
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25-MAR-2003
31-OCT-2002
                                                            23-SEP-1987
                                      EP237676-A.
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                                                                                                                                                         Piatak M;
          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                             96 BLSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 BLSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                    36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                   0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of Ricinus communis castor beans ricin toxin (RT or ricin) A protein encoded by pRA123.
                                                                                                                                                                                                                        N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                         Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                                                              97.9%; Score 951; DB 8; Length 332;
94.9%; Pred. No. 1.7e-93;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                      Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70838 standard; protein; 332 AA.
                                                                                                                                                                      Chang S,
                                                                                                                                                                                                                                                       Disclosure; Fig. 4; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOYIEGEMRIRIRYNRRS 189
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/note="Leader"
                                                                                                                 86US-0860330.
85US-0778414.
            Ricin A; Met-aminopeptidase.
                                                                                             86EP-0307242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 94.99
Matches 188, Conservative
                                                                                                                                                                      Benbassat A, Bauer KA,
                                                                                                                                                                                         WPI; 1987-110172/16.
N-PSDB; AAN70152.
                                                                                                                                                 (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                           332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricinus communis.
                                Escherichia coli.
                                                                                                                  06-MAY-1986;
20-SEP-1985;
                                                                                             19-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant toxin.
                                                                         22-APR-1987
                                                     EP219237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
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                                                                                                                                                                                                                                                                                                             Sequence
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obten using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three plasmids contg. CDNA inserts obtain a CDNA library for sequences encoding ricin B using the probe in AAN70517. The CDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a Hindlif site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression (vectors contg. the PhoA promoter-Operator and leader sequence (AAN70523) and sultable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 951; DB 8; Length 332; 94.9%; Pred. No. 1.7e-93; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 FQYIEGEMRTRIRYNRRS 233
/note="A-chain"
315..332
/note="B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                  86EP-0308877
                                                                                                                                                                                                                                                                                                                                                    86US-0837583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1987-265177/38.
N-PSDB; AAN70519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                  13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                       07-MAR-1986;
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96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenfield L, Nitecki D, Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%; Score 951; DB 10; Length 332; 94.9%; Pred. No. 1.7e-93; rive 0; Mismatches 0; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                   Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
                         Ricin A encoded by insert from plasmid pRA123.
                                                                                                                                  ..35
label= leader sequence
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gelfand D, Lawyer FC, Horn G,
                                                                                                                                                                                                                           /label=B-chain
                                                                                                                                                                        /label=A-chain
                                                                                                                                                                                                /label=linker
                                                                                                                                                                                                                                                                                                                                   84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                                                                                                           89EP-0201162.
                                                                                                                                                                                                                                                                                                                                                                                                                 CORPORATION.
13-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 94.9
nes 188; Conservative
                                                                                                                                                         .302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 AA;
                                                                              Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN91281
                                                                                                                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS
                                                                                                                                                                                                                                                                                                           19-JAN-1989;
                                                                                                                                                                                                                                                                                                                                    08-FEB-1984;
08-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                19-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             host cells.
                                                                                                                                                                                                                                                                                04-OCT-1989
                                                                                                                                                                                                                                                     EP335476-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piatak MJ;
                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                               Peptide
                                                                                                                                                          Peptide
                                                                                                                                                                                   Peptide
                                                                                                                                                                                                               Peptide
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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histatidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. Coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                        Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 97.9%; Score 951; DB 16; Length 554; Best Local Similarity 94.9%; Pred. No. 3.4e-93; Matches 188; Conservative 0; Mismatches 0; Indele 10
                                                                                                                                                                                                                                                                                                                                           'note= "MAb 4197X heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood MS;
                                                                                                                                                                                                                                                                                                      "phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                         /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                        549..554
/label= TAG
/note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                   ...27
/label= Sig_peptide
                                                                                  AAR70827 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            label= RICIN-A
172 POYIEGEMRIRIRYNRRS 189
            216 FOXIEGEMETRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                  /label= LINKER
                                                                                                                                                                                                                                                                                                                   28..145
/label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0101329.
                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                     Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                .544
                                                                                                                                                                                                                                                                                                                                                      166
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                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ85386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9503828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-1995.
                                                                                                                                   25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                            AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                     Domain
                                                              RESULT 8
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96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                          112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L5-JUL-1983;
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                                                                                                                                                                                                                                                                        16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP145111-A.
                                                                                                                                                                                                                                          AAP50166;
                                                                                                                                                                                                                                                                                                                                                                 Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                               RESULT 10
AAP50166
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                                                                            g
                                                                                                           à
                                                                                        338 BLSNHAELSVTLALDVINAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 397
                                                                                                                         112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                          398 GNYDRLEQLAGNLRENIELGNGPLEEAISALXYYSTGGTQLPTLARSFIICIQMISEAAR 457
                                                              52 ELSNHAELSVTLALDVTNAVVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                               278 IFPKQYPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 337
         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 951; DB 10; Length 562;
Pred. No. 3.5e-93;
0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
            2 IFPKOYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                            AAP90079 standard; protein; 562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; fig 1; 51pp; English
                                                                                                                                                                                                       Ricinus communis (caster beans)
                                                                                                                                                                                       172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.9%;
Best Local Similarity 94.9%;
Matches 188; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88WO-US04238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87US-0124735
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                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown EL, Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN90068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO8904839-A.
                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1989
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                                                                                                                                                                                                                                                                                                                       AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                 Ricin D.
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52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111

36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95

g ð

à

IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLT--

51

---VLPNRVGLPINQRFILV

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Preproricin is the whole polypeptide encoded by AAN50202 and the DNA encoding this is claimed. Proricin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
                                                                                                                                                                                                                                                                                                                      292..303
/label= links the C-terminus of the A chain and
the N-terminus of the B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA sequences coding for ricin type plant toxin - mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                               398..400
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                         'label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                      260..262
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-linked glycosylation
                                                                                                                                                                                               Sequence of preproricin encoded by pRCL617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 30-30c; 40pp; English.
                                                                                                                                                                                                                                                                          cocation/Qualifiers
                                                                                                                        Ŗ.
                                                                                                                        AAP50166 standard; Protein; 565
                                   172 FOYIEGEMRIRIRYNRRS 189
                                                    216 FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                 /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84GB-0006569.
83GB-0019265.
83CH-0019265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84EP-0304801
                                                                                                                                                                                                                        Foxin; anti-tumour therapy
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    438..440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYWA-) UNIV WARWICK.
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                                                                                                              52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                      144
                                                                                                                                                            112 GNYDRLEQLAGNLRENIELGNGPLEFAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition comprising toxin e.g., ricin based antiviral compound 1 for treating viral infections such as human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303..565
/label= Ricin B chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                    25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV 84
                                                                                                                                 Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                 97.9%; Score 951; DB 6; Length 565;
94.9%; Pred. No. 3.5e-93;
.ive 0; Mismatches 0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291..302
/label= Linker peptide
/note= "Cleaved during activation of ricin"
                                                                                                                                                                                                                                                                                                                                                                       Castor bean preproricin protein (SEQ ID 1).
                                                                    2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..24
/label≈ Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25..290
/label= Ricin_A_chain_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                   AAG78300 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                                                                 FOYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                      205 FOYIEGEMRTRIRYNRKS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                               Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-581908/65.
                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI64137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus communis.
565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                    15-NOV-2001
                                                                                                                                                                                                                   172
                                                                                                                                                                                                                                                                                                                             AAG78300;
  Sequence
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel
                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                          AAG78300
                                                                                                                                                                                                                                                                                                                 엄
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The sequence relates to preproricin protein encoded by the DNA sequence given in Al64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HTV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The residues on cell surfaces, and its cellular internalisation. The and other viral infections, especially retroviral infections and other viral infections in viral particles or early-stage infected antiviral agent is activated in viral particles or early-stage infected antiviral agent is activated in viral particles or early-stage infected integration of the viral spenome into the host genome thereby preventing the latency/rebound problem. The agent enters all HTV susceptible cells, and one just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Proricin consists of the ricin A chain, a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide, and the ricin B chain. Proridin is proteclytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                             2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                     25 IFPKQYPIINFTTAGAIVQSYINFIRAVRGRLTTGADVRHDIPVLBNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castor bean plant; preproricin, ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels 10;
                                                                                                                                                                                                                                                                                                                                          Length 565;
                                                                                                                                                                                                                                                                                                                                            Score 951; DB 22;
Pred. No. 3.5e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292..303
/label= Linker_peptide
296..297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25..291
/label= Ricin A chain
/note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG78304 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25..565
/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 FQYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 FQYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                  97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                   565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG78304;
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG78304
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Cleavage-site

Disclosure; Page 47-50; 66pp; English.

virus infection.

25-MAR-2003

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The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to a virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virus the activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                  304..565
/label= Ricin B chain
/note= "GalacToSe/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 97.9%; Score 951; DB 22; Length 565; Best Local Similarity 94.9%; Pred. No. 3.5e-93; Matches 188; Conservative 0; Mismatches 0; Indels 10
/label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                          (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                             15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                  16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                                Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                       WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 AA;
                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                                                                                                                                                                          virus infection.
                                                                                                WO200160393-A1
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AAP70326
ID AAP70:
XX
AC AAP70
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AAP70326 standard; Protein; 576 AA.

AAP70326;

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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a CDNA library, and then probing the library to retrieve the RNA to obtain a CDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see plasmids containing cDNA inserts of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the AbA promoter-operator and leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 GNYDRLEQLAGNERENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ELSNHAELSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 576;
                                                                                           Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                            Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.9%; Score 951; DB 8;
94.9%; Pred. No. 3.6e-93;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAN70523) and suitable retroregulators. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 14(1-2); 112pp; English.
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                        /note= "A-chain"
315..576
/note= "B-chain"
                                                                                                                                                                                                         /note= "leader"
                                                                                                                                                                                                                                                                                                                                                                       86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                       86US-0837583.
(updated)
(first entry)
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                                                                                                                                                                                                                            36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1987-265177/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 AA;
                                                                                                                                            Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN70526.
                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                          23-SEP-1987.
                                                                                                               plant toxin
                  21-MAY-1991
                                                                                                                                                                                                                                                                                                          EP237676-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                             Region
                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                            Region
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156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see Arr91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B' interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation demain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New hybrid molecules for delivery of agents to cells - comprise binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                  Ricin, cytotoxin, hybrid protein, cell delivery; cell binding ligand; translocation domain, diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 11A-B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                     ...35
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                          AAW25787 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                              36..302
/label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                      315..576
/label= B-domain
                          FOXIEGEMRTRIRYNRRS 189
                                                216 FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                           303..314
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-0722484.
84US-0618199.
85US-0726808.
85US-0742554.
89US-0456095.
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                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-470103/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SERA-) SERAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT91638.
                                                                                                                                                                                                                                                                                                            Ricinus communis.
                                                                                                                                                                                                                           Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1993;
                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5668255-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1997
                                                                                                                                                                                               27-MAR-1998
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                           172
                                                                                                                                                      AAW25787;
                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                 RESULT 14
                                                                                                              AAW25787
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111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 IFPKGYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant, hybrid, binding domain, ligand, animal cell; diphtheria, translocation domain, botulinum; neurotoxin, ricin; cholera, tetanus; shiga-like toxin, pertussis, translocation, cytoplasmic membrane; HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.9%; Score 951; DB 18; Length 576; Best Local Similarity 94.9%; Pred. No. 3.6e-93; Matches 188; Conservative 0; Mismatches 0; Indels 10
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22-DEC-1989;
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therapy to affected cells, allowing them to function properly and allewiate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precureor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells. The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polygeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein toxin, proxin, IT toxin, C3 toxin, botulinum neurotoxin, ricin, cholera toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the call, which is non-native to the naturally occurring protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate Example 4; Fig 11; 31pp; English.

576 AA; Seguence

1; 21 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 0; Indels 10; Gaps Query Match 97.9%; Score 951; DB 20; Length 576; Best Local Similarity 94.9%; Pred. No. 3.6e-93; Matches 188; Conservative 0; Mismatches 0; Indels 1 à

96 ELSNHABELSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155 52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111 36 IFPKÓYPIINFTTAGATVÓSYTNFIRÁVRGRLÍTGADVRHEIPVLPNRVGLPINQRFILV 95 d δ g

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Search completed: February 10, 2004, 16:22:27 Job time : 33.2239 secs

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Sequence 74, Appl
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                                                                         February 10, 2004, 16:18:30; Search time 10.9281 Seconds (without alignments) 731.761 Million cell updates/sec
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1 MIFPKQYPIINFTTAGATVQ.....ARFQYIEGEMRTRIRYNRRS 189
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Patent No. 52
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3: \cgg12_6\ptodata1/iaa\6A_COMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-356-786-10

US-07-988-430-1

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US-08-425-336-1

US-08-4477-484B-1

US-08-4477-484B-1

US-08-646-360-1

US-09-610-838-1

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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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		Application 897305 FORMATION: 1: Huston, 1: Opperman 1: Ning, Da 1: Ring, Da 1	Ë
		-786-8 8 9, 53 No. 5 39 No. 5	
336 336 336 336 337 320.5 310.5 310.5 310.5 305 305 305 305 305 305 305 305 305 30		T 1 -356-786-8 Buence 8, Application ent No. 587705. MERAL INNCRMATION: APPLICANT: Huston, APPLICANT: Hoston, APPLICANT: Ring, Da APPLICANT: Ring, Da APPLICANT: Ring, Da APPLICANT: Ring, Da TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: STREET: Exchange COUNTRY: USA ZIP: MASSACHUSE COUNTRY: USA ZIP: MASSACHUSE COUNTRY: USA ZIP: ASSACHUSE COUNTRY: USA ZIP: OSTONE TELE ON TOWNER FILING DATE: OG-F FILING DATE: OG-F FILING DATE: OG-F REIGNATION INWERF FILING DATE: OG-F REIGNATION INWERF FILING DATE: OG-F REGISTRATION INWERF REFERRICE/OMOCKET IN TELECOMMUNICATION IN TELEFRAX: (617) 24 REGISTRATION FOR SEQ ID SEQUENCE CHARACTERIS LENGTH: Z68 amino acid TYPE: amino acid TYPE: prot	벌병
		HESULT 1 US-08-356-786-8 Sequence 8, Application Sequence 8, Application BAPPLICANT: Huston, APPLICANT: Huston, APPLICANT: Houston, APPLICANT: Ring, ITILE OF INVENTION TITLE OF INVENTION STARET: Exchange CITY: Boston STARET: Exchange CITY: Massachum STARET: Exchange CITY: Massachum STARET: Exchange CONPUTER: EDMP CONPUTER: EDMP COMPUTER: EDMP SOFTWARE: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent SOFTWARE: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent COMPUTER: Patent SOFTWARE: Patent COMPUTER: Patent CO	Query Ma Best Loc Matches
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                                                                   63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                          171 RFQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                      Sequence 1, Application US/07901707
Patent No. 5376546
                                                                                                                                                                    183 RFOYIEGEMRTRIRYNRRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAONE: (312) 346-5750
TELEPAX: (312) 984-5750
TELERX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 267 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: US?
ZTD.
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-901-707-1
                                                                                                                                                                                                                                                         US-07-901-707-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 MIFPKÓYPIINFTTAGATVÓSYTNFIRAVRGRLÍTGADVRHEIPVLPNRVGLPINQRFIL 62
                                                                                       VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 110
                                                                                                                               61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                                                                                                        111 GGNYDRLEQ1AGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 170
                                                                                                                                                                                              1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermenn, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. Edmund R. Pitcher, Testa, Burwitz, & Thibeault
Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.5%; Score 956; DB 2; Length 534; 95.0%; Pred. No. 2e-102; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
          MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: CRP-053
TRIBERENCE/DOCKET NUMBER: CRP-053
TRIBECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILLING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                171 RFQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                 181 RFOYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 amino acids
nino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.0°
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Excura-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-356-786-10
                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-356-786-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
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APPLICANT: Berthard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
CORRESPONDENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYFFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.9%; Score 951; DB 1; Length 267; Best Local Similarity 94.9%; Pred. No. 2.7e-102; Matches 188; Conservative 0; Mismatches 0; Indels 1
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61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                  121 GNYDRLEQLAGN.RENIELGNGPLEEAISALYYYSTGGTQL.PTLARSFIICIQMISEAAR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Gaps
                                                                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois COUNTRY: USA ZIPE 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILMS DATE: 18-APR-1995
CLASSIFICATION TOWNER: 08/064,691
APPLICATION NUMBER: 08/064,691
FILMS DATE: 12-MAY-1993
APPLICATION NUMBER: US/07/901,707
FILMS DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILMS DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 951; DB 1; I
Pred. No. 2.7e-102;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-36,989
                                                                                                                                                                                                                                   Sequence 1, Application US/08425336 Patent No. 5621083
                                                                                                                            181 FÓYIEGEMRTRIRYNRRS 198
                                                                                     172 FOYIEGEMRIRIRYNRRS 189
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ilarity 94.9%;
Conservative
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REGISTRATION NUMBER: P-3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 267 amino acids
amino acid
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312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 188; Conserva
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                             RESULT 5
US-08-425-336-1
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ELSNHAELSVILALDVINAVVGYRAGNSAVFFHPDNQEDAEAITHLFTDVQNRVIFAFG 120
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                      121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels 10; Gaps
  Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
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Pred. No. 2.7e-102;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION UNBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NO. 5416202and, Greta E. REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                               US-07-988-430-1
; Sequence 1, Application US/07988430
Patent No. 5416202
; GENERAL INFORMATION:
                                                                   172 FQYIEGEMRTRIRYNRRS 189
                                                                                                          181 FOYIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-07-988-430-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bicknell
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Illinois
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Best Local
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PRIOR SEPTIALITY: 30.9

PRIOR SEPTIALITY: 30.9

PRIOR APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MX-1993

PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/797,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION: NAME: MCNICHOLAS, Jane MCNICHOLAS, Jane MCNICHOLAS, Jane MCNICHOLAS, Jane MCNICHOLAS, Jane MCNICHOLAS, JANE MERERNEE/DOCKET MUMBER: 32,918

REFERENCE/DOCKET MUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                      172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312/707-9153
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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STATE: Illinois
COUNTRY: USA
ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                            US-08-477-484B-1
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2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------ULPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary, Gary
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF EXQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%; Score 951; DB 1; Length 267; 94.9%; Pred. No. 2.7e-102; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARACTION NUMBER: US/08/488,113B
PELLING DATE: 07-JUN-1995
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 6661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                Sequence 1, Application US/08488113B Patent No. 5744580 GENERAL INFORMATION:
                                                                                                                            181 FOYIEGEMRTRIRYNRRS 198
                                                                                172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 amino acids
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Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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61 ELSNHAELSVITLALDVINAXVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 120
                                                                112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                              APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-UNN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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97.9%; Score 951; DB 1; Length 267;

Query Match

1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60

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97.9%;
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                                                                                                                                                           Matches 188; Conservative
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-1
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ADDRESSEE: Multiple STREET: 500 West Multiple CITY: Chicago "MATE: Illinois
                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                             52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                     112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                               1 IFPKQYPIINPTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                     -----VLPNRVGLPINQRFILV 51
                            Gaps
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Patent No. 5837491

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,430
FILING DATE: 09-DEC-1992
  94.9%; Pred. No. 2.7e-102; cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                         2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                      181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MCNicholas, Janet M. REGISTRATION NUMBER: 32,918 REFERENCE/DOCKET NUMBER: 2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELES: 650 388-124
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
  Best Local Similarity 94.9
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDAL
STREET: buc
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-646-360-1
                                                                                                                                                                                                                                                                                                                                                172
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                          52 ELSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFG
                                                                                                                                                                  1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV
                                                       0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studmika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
  Length 267;
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
Score 951; DB 2; I
Pred. No. 2.7e-102;
                                                             0; Mismatches
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
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ATTORNEY/AGENT INFORMATION:
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Patent No. 6146631
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 FOYIEGEMRIRIRYNRRS 189
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US-09-610-838-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                             1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                    --VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENITON: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENITON: Proteins
NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                  Query Match
97.9%; Score 951; DB 3; Length 267;
Best Local Similarity 94.9%; Pred. No. 2.7e-102;
Matches 188; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
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APPLICATION NUMBER: US/09/136,389
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Patent No. 6146850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FOYIEGEMRTRIRYNRRS 198
TELEPHONE: 312/707-8889
TELERA: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE MCANDESS: 173
CORRESPONDENCE MCANDESS: ADDRESS:
ADDRESSEE: MCANDESWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.9%; Score 951; DB 3; Length 267; 94.9%; Pred. No. 2.7e-102; Artive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
                  APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANACOLAB, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEFROM 312/707-8899
TELEFAX: 312/707-8899
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09610838 Patent No. 6376217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.99
Best Local Similarity 94.99
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-09-136-389-1
PRIOR APPLICATION DATA:
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Illinois
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OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                        CONTRACT AFELLIAN NUMBER: PCT/US92/09487
CLASSIFICATION NUMBER: PCT/US92/09487
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
                                                                          ыыык: PCT/US92/09487
19921104
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION: TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 POYIEGEMRTRIRYNRRS 189
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    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WALSH, TERENCE A APPLICANT: HEY, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOMF
TITLE OF INVENTION: PRECURSC
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-09487-1
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Best Local Similarity
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%; Score 951; DB 4; Length 267; 94.9%; Pred. No. 2.7e-102; ive 0; Mismatches 0; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UON-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UON-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGRAT INFORMATION:
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: 312/707-9889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9209487
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISITCS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 267 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.9<sup>3</sup>
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US92-09487-1
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                     61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNOEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                      52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                   2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 51
                                                                                                                                               1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                    10; Gaps
97.9%; Score 951; DB 5; Length 267; 94.9%; Pred. No. 2.7e-102;
                                                 0; Indels
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Search completed: February 10, 2004, 16:29:32
   ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                   Length 290;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: BORUCKI, ANDRER: 38651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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Pred. No. 3e-102;
0; Mismatches 0
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FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE
                                                                                                                                                                                                                                                                                                                                                                                     97.9%;
                                                                                                                                                                                                                                                 LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.9
Matches 188; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                US-08-378-761A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-485-286-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 951; DB 1; Length 290; 94.9%; Pred. No. 3e-102; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Patent No. 5248606
; APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
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0; Mismatches
          REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELEPHONE: OSTON INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 anino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 FQYIEGEMRTRIRYNRRS 189
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BORUCKI, ANDREA T
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.9%
Matches 188; Conservative
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                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-485-286-27
                                                                                                                                                                                                                          STRANDEDNESS: single
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Job time : 10.9281 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

(without alignments) 1623.314 Million cell updates/sec February 10, 2004, 16:26:46; Search time 24.3781 Seconds

US-10-083-336A-6

1 MIFPKQYPIINFTTAGATVQ........ARFQYIEGEMRTRIRYNRRS 189 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

801455 segs, 209382283 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Seguence 6, Appli	Sequence 11, Appl	Sequence 4, Appli	Seguence 8, Appli	Sequence 5, Appli	Sequence 10, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 2, Appli	Sequence 39, Appl
ŒΙ	US-10-083~336A-6	US-10-083-336A-11	US-10-083-336A-4	US-10-083-336A-8	US-10-083-336A-5	US-10-083-336A-10	US-10-083-336A-3	US-10-127-890-1	US-10-083-336A-1	US-10-083-336A-7	US-10-282-935-1	US-10-440-796-1	US-10-083-336A-9	US-10-083-336A-2	US-09-792-793A-39
ВО	12	12	12	12	13	12	12	12	12	12	12	12	12	12	10
% Query Match Length DB	189	190	188	188	199	200	198	267	576	198	267	267	185	179	247
% Query Match	100.0	100.0	99.5	98.5	98.5	98.5	97.9	97.9	97.9	6.96	6.96	6.96	96.8	6.69	34.6
Score	971	971	996	926	956	926	951	951	951	941	941	941	939.5	619	336
Result No.	н	7	٣	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15

181 TRIRYNRRS 189

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Sequence 6, Appli Sequence 39, Appl Sequence 4, Appli	Sequence 34, Appl Sequence 34, Appl	m r	,,	4,	'n	Sequence 2, Appli	1,7	Sequence 106, App	•	7	247	Sequence 2, Appli	99	10		10	Sequence 103, App	104,	Sequence 105, App	Sequence 1, Appli	Seguence 11, Appl			Sequence 253, App
12 US-10-127-890-6 12 US-10-375-209A-39 12 US-10-280-679B-4	10 US-09-792-793A-34 12 US-10-375-209A-34	12 US-10-282-935-3	12 US-10-127-890-7	12 US-10-127-890-4	12 US-10-127-890-5	9 US-09-347-064-2	12 US-10-127-890-107	12 US-10-127-890-106	12 US-10-127-890-110	12 US-10-127-890-111	9 US-09-765-527-247	12 US-10-127-890-2	12 US-10-127-890-99	12 US-10-127-890-100	12 US-10-127-890-101	12 US-10-127-890-102	12 US-10-127-890-103	12 US-10-127-890-104	12 US-10-127-890-105	12 US-10-074-596-1	12 US-10-074-596-11	12 US-10-127-890-109	9 US-09-765-527-259	9 US-09-765-527-253
247 247 289	247	251	263	263	248	252	251	251	251	251	251	251	251	251	251	251	251	251	251	316	507	251	293	309
34.6 6.4.6	31.4	30.6	28.1	28.0	26.5	26.2	25.3	25.2	25.2	25.2	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.0	25.0	25.0
336 336 336	305	297.5	27.5	272	257.5	254	245.5	244.5	244.5	244.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	242.5	242.5	242.5
16 17 18	119	27	23	24	25	26	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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61 VILALDVINAXVVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYTFAFGGNYDRLEQL 120
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael P
CURRENT APPLICANTION RICHAEL AND APPLICANTION RICHAEL AND APPLICANTION RICHAEL AND APPLICANTION NUMBER: US/10/083,336A
CURRENT PILING DATE: 2002-05-21
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ricinus communis
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US-10-083-336A-6
US-10-083-336A-6
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1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSV 60
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US-10-083-336A-5
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: 867452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
                                                                                                             US-10-083-336A-11
Sequence 11, Application US/10083336A
Sequence 11, Application US/10083336A
Publication No. US2030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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100.0%; Pred. No. 2.7e-103;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 188; Conservative
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Best Local Similarity 100.0
Matches 189; Conservative
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SEQ ID NO 11
LENGTH: 190
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181 TRIRYNRRS 189
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63 ALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN 122
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                                   61 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
                                                                                                                                                    62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                    122 GNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
TITLE OF INVENTION Ricin Vaccine and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT TILING DATE: 2002-05-21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSVTL 62
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Local Similarity 100.0%; Pred. No. 1.4e-101;
hes 186; Conservative 0; Mismatches 0; Indels
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APPLICANT: Olson, Mark A
APPLICANT: Byrne, Michael B
APPLICANT: Byrne, Michael F
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods
FILE REFERENCE: F67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                    61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
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Publication No. US20030181665A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Mainementer, Robert W
APPLICANT: Wannementer, Robert W
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael V
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                           0; Indels 10;
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                                                                                        Score 956; DB 12; Length 199;
Pred. No. 1.5e-101;
                                                                                                                                             0; Mismatches
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                                                                                        98.5%;
95.0%;
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TYPE: PRT ORGANISM: Ricinus communis
                                                                                                                                           Matches 189; Conservative
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                                                                                             Query Match
Best Local Similarity
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                                ; ORGANISM: RIC
US-10-083-336A-5
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LENGTH: 200
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; Sequence 3, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:

US-10-083-336A-3

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61 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 İFPKQYPİINFTTAGATVQSYTNFIRAVRGKLTTGADVRHEIPVLPNRVGLPINQRFILV 60
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Chael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
TILLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARR: PATENTING DATE: 2002-05-21
SOFTWARR: PATENTING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 10;
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COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION LOWNER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: L2-MAY-1994
APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 951; DB 12;
Pred. No. 5.7e-101;
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.9%;
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 198
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Sequence 7, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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                                                                                                                                      172 POYIEGEMRTRIRYNRRS 189
                                                                                                                                                                 216 FQYIEGEMRTRIRYNRRS 233
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Best Local Similarity
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
FILE REFERRACE: P67452USO (RIID 01-58)
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.9%; Score 951; DB 12; Length 267; Best Local Similarity 94.9%; Pred. No. 8.7e-101; Matches 188; Conservative 0; Mismatches 0; Indels 10
                 FILING DATE: 19-JUN-1992
APPLICATION WINBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONIACIOLAS, JAMEE M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEFOMMUNICATION INFORMATION:
TELEFOMMUNICATION INFORMATION:
TELEFOMMUNICATION 12/707-8889
TELEFAX: 312/707-9155
TELEFAX: 312/707-9155
TELEFAX: 312/707-9155
TELEFAX: SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 FOYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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APPLICANT: UTETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD: 884US
CURRENT APPLICATION NUMBER: 05/10/282,935
CURRENT FILING DATE: 2002-10-29
FRIOR PILING DATE: 2000-03-30
FRIOR APPLICATION NUMBER: 60/126,826
FRIOR APPLICATION NUMBER: 60/126,826
FRIOR PILING DATE: 12000-03-30
FRIOR PILING DATE: 2000-03-30
FRIOR PILING DATE: 2000-03-30
FRIOR FILING DATE: 2000-03-30
FRIOR FILING DATE: 12000-03-30
FRIOR FILING DATE: 2000-03-30
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                                                                                                                            96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                        112 GNYDRLEQLAGNIRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michel P
APPLICANT: Byrne, Michel P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERBNCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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123 YDRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
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                                                                                                                                                                                                         ; Sequence 9, Application US/10083336A; Publication No. US20030181665A1
                                                174 YIEGEMRTRIRYNRRS 189
                                                                                            183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                        FULLICATION NO. US20030181665A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               APPLICANT: Olson, Mark A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 RIRYNRRS 189
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US-10-083-336A-9
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APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
APPLICANT: GHETIB, VICTOR F.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: COMPOSITIONS (VLS)
FILE REPERENCE: UTSD: 603
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT FILING DATE: 2003-05-19
FRIOR PLING DATE: 2000-03-30
FRIOR PLING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 1999
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO.
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                                                                                                                                                                                                                                                          Gaps
                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                           Query Match

96.9%; Score 941; DB 12; Length 267;
Best Local Similarity 94.9%; Pred. No. 1.2e-99;
Matches 186; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: CTHER INFORMATION: Peptide US-10-440-796-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 941; DB 12;
Pred. No. 1.2e-99;
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Best Local Similarity 94.9%;
Matches 186; Conservative
  SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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58 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 117
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEO ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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96.8%; Score 939.5; DB 12; Length 185;
Best Local Similarity 98.4%; Pred. No. 1.1e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.9%; Score 679; DB 12; Length 179; 93.1%; Pred. No. 9e-70; ive 0; Mismatches 0; Indels 10
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RESULT 15

US-09-792-792-934-39

Sequence 39, Application US/09792793A

Sequence 39, Application US/09792793A

Sequence 39, Application US/09792793A

Patent No. US20020168370A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: McDonald, John R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

TITLE OF INVENTION NUMBER: US/09/792,793A

CURRENT APPLICATION NUMBER: US/09/792,793A

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93

SSOFTWARE: Patentin Ver. 2.0

SSOF ID NO 39

LENGTH: 247

TITLE OF STATE PATE TRICHOSANTHEWS KITILOWII

US-09-792-793A-39
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                                                                                                                                                                    96 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                                                                52 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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2 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 INFTTAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 59
                                 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 34.6%; Score 336; DB 10; Length 247; Best Local Similarity 38.9%; Pred. No. 3.7e-30; Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps
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                                                                                                                                                                                                                              112 GNYDRLEQLAGNLRENIELGNGPL 135
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171 IGKRV 175
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 10, 2004, 16:17:35; Search time 10.2276 Seconds (without alignments) 1777.145 Million cell updates/sec

US-10-083-336A-6

971 1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 189 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTTANATO

		oko (SUMMARIES	
Kesult No.	Score	Query	Length	DB	ΩI	Description
	951	97.9	576		RLCSD	ricin D precursor
7	861.5	88.7	564	Н	RLCSAG	tin
m	336	34.6	289	Н	RLTZT	rRNA N-qlycosidase
4	327.5	ω,	528	7	532431	abrin-d precursor
Ŋ	327.5	33.7	562	N	S16022	abrin-c precursor
ø	326	33.6	247	7	JU0393	karasurin - Mongol
7	326	33.6	247	7	JC5032	karasurin-B - Tric
æ	326	33.6	289	~	JC5606	karasurin C - Tric
σ	323	33.3	527	7	S32430	abrin-b precursor
10	310.5	32.0	251	7	C39761	abrin (clone 7.2)
11	303.5	31.3	528	Н	TZLSA	abrin-a precursor
12	300.5	30.9	278	7	823519	beta-luffin - smoo
13	293.5	30.2	250	7	JN0108	lúffin-b - smooth
14	274.5	28.3	277	7	S22494	rRNA N-glycosidase
12	273	28.1	286	1	RLPUGG	rRNA N-glycosidase
16	273	28.1	570	~	862627	agglutinin I precu
17	272	28.0	286	7	S25560	rRNA N-glycosidase
18	270		245	N	JC4840	rRNA N-glycosidase
13	265	27.3	286	N	JC4235	rRNA N-glycosidase
20	264	27.2	254	7	PD0018	mistletoe lectin I
21	243.5		316	7	JT0753	rRNA N-glycosidase
22	186.5	19.2	294	7	S28421	rRNA N-glycosidase
23	~		278	N	A39817	rRNA N-glycosidase
24	170	17.5	313	2	S17757	rRNA N-glycosidase
25	æ		261	7	JE0401	antiviral protein
56	4		289	7	T12573	rRNA N-glycosidase
27	138	14.2	272	2	JC4811	betavulgin - beet
28	131		253	7	S28542	rRNA N-glycosidase
29	127	13.1	253	7	S28539	rRNA N-qlycosidase

rRNA N-glycosidase ribosome-inactivat	rRNA N-glycosidase rRNA N-glycosidase rRNA N-glycosidase	rRNA N~glycosidase tritin - wheat	rRNA N-glycosidase rRNA N-glycosidase	protein synthesis rRNA N-glycosidase	hypothetical prote shiga-like toxin I	Shiga toxin 2 subu Shiga toxin 2 subu	Shiga-like toxin I
\$29931 \$46239	S05205 S28541 RLQHG2	S17519 S33631	A58923 RLBH	JC5848 S17932	S21940 I54695	E90779 G85640	S01032
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310	283 253 292	293	253	280	319 319	319	318
13.1	12.8 12.7	12.0	11.8	11.5	11.2	11.1	11.1
127	124 123 121	116.5	115	112	109	108 108	107.5
30	3 8 8 4 8 8	36	37 38	0.4 0.0	41 42	44 44	45

ALIGNMENTS

RESULT 1 RLCSD
ricin D precursor - castor bean N;Contains: rRNA N-qlycosidase (EC 3.2.2.2)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A, Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A; Reference number: A24041; MUID: 86067214; PMID: 2999712
A;Accession: A24041
A;Molecule type: DNA
A;Residues: 1-576 <hal></hal>
A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083
R;Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A, Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a
A; Reference number: S20513; MUID:92163016; PMID:1371405
A;Accession: S20513
A; Molecule type: DNA
A:Residues: 1-576 <tre></tre>

A.Kestaudes: 1-5/N c/KED.
A.Kestaudes: 1-5/N c/KED.
A.KTCOSS-references: EMBL:K52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
R.Lamb, F.I.; Roberts, L.M.; Lord, J.M.
R.Lamb, F.I.; Roberts, L.M.; Lord, J.M.
A.K. Biochem. 148, 265-270, 1985
A.Jitle: Nucleotide sequence of cloned cDNA coding for preproricin.
A.Keference number: A24614; MUID:85179479; PMID:3838723

A; Accession: A24614

A;Molecule type: mRNA A;Residues: 12-75, 10', 77-550, R',522-576 <LAM> A;Residues: 12-75, 10', 77-550, R', 1521077; PIDN:CAA26230.1; PID:g21078 A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 R;Yoshitake, S.; Funatsu, G.; Punatsu, M. R;Yoshitake, S.; Funatsu, G.; Punatsu, M. A;Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile challence number: A03372

A; Accession: A03372

A,Molecule type: protein
A,Residues: 36-97, 0',99-109, 'S',111-269,'D',272-283,'L',285-288,290-302 <YOS>
A,Residues: 36-97, 0',99-109, 'S',111-269,'D',272-283,'L',285-288,290-302 <YOS>
A,Note: this paper cites the others in the series providing experimental details for the R;Arsi, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A,Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A; Reference number: A24010 A; Accession: A24010

A; Molecule type: protein A; Residues: 315-383, PS', 386-576 <ARA> A; Residues: 315-383, PS', Reliantsu, M. Frunatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A; Title: Primary structure of Ala chain of ricin D.

A; Reference number: A03374

A;Accession: A03374 A;Molecule type: protein

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A; Molecule type: mRNA
A; Residues: 1-289 < SHA>
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A; Contents: annotation; A:ray crystallography, 2: angestroms
C; Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subu
nto the cell of the A chain; B chains are also responsible for cell agglutination (lecti
C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Superfamily: ricin; RNA M-91ycosidase homology
C; Keywords: duplication; glycoprotein; glycop
A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',4d557,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>A;Note: this paper, one of a series, summarizes the experimental details for the determi R;Ready, M.P.; Kim, Y.; Robertus, J.D.
                                                                                                                                                                                          Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism
A;Reference number: A48237; MUID:91352006; PMID:1881883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Contains: rRNA N-glycosidase (EC 3.2.2.2)
(Species: Ricinus communis (castor bean)
(Species: Ricinus communis (castor bean)
(Species: 13-Dec-1993 #text_change 16-Jul-1999
(Spacession: A24261, A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-1586, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A;Reference number: A24261; MUID:86059449; PMID:2999130
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A;Residues: 1-564 <ROB>
A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
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A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Reference number: A48238; MUID:91352005; PMID:1881882
A;Contents: annotation, X-ray crystallography, 2.5 angstroms R;Kazin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Reference number: A48239; MUID:91352004; PMID:1881881
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Best Local Similarity 94.9%; Pred. No. 2.7e-79;
Matches 188; Conservative 0; Mismatches 0;
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A, Molecule type: protein

A, Residues: 303-325, F', 327-330, T', 332-361, D', 363-373, G', 375-403, T', 405-551, VV, 553-

C, Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C, Superfamily: ricin; rRNA N-glycosidase homology
C, Reywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F; 12-24/Domain: signal sequence #status predicted <5GS-
F; 15-281/Domain: signal sequence #status predicted <ACH>
F; 25-281/Domain: rNA N-glycosidase homology <RNG-
F; 303-564/Product: agglutinin chain B #status predicted <ACH>
F; 303-564/Product: agglutinin chain B #status predicted
F; 304-558 Binding site: carbohydrate (Asp) (covalent) #status predicted
F; 304, 259 Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 305, 204, Arciive site: Glu, Arg #status predicted
F; 205, 203/Arciive site: Glu, Arg #status predicted
F; 224, 337, 348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted
F; 324, 337, 348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
F; 397, 437, binding site: Carbohydrate (Asn) (covalent) #status predicted
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R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Blochim. Blophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti)
A;Reference number: A24210
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C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-59-1988 #sequence revision 2-dan-1996 #text_change 23-Mar-2001
C;Accession: JTO566; A36274; JC1093; A36273; JT0003
R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
A;Reference number: JT0566; MUID:91153657; PMID:1999291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-233,'T',235-246,'M',248-289 <CHO>
A;Cross-references: GB-105434, NID:9170534; PIDN:AAA34206.1; PID:9170535
R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A;Reference number: JC1093; MUID:94271613; PMID:8003348
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A; Accession: JT0003

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Cydate: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
CyAccession: S32431; S34408
RyHung, C.H.; Lee, M.C.; Lin, J.Y.
Nol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32431
A;Residues: 1-528 <HUN>
A;Cross-references: GB:M98346
A;Cross-references: GB:M98346
B;Hung, C.; Lee, M.; Lee, T.; Lin, J.
Submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating. The A and B chains are linked by a single disulfide bond, which is essential for toxicit C;Superfamily: rich; rRNA N-glycosidase homology C;Reywords: disulfide bond, duplication; glycoprotein; glycosidase, hydrolase; lectin; py F;1-251/Product: abrin-d chain A #status predicted ACH>
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Bur. J. Biochem. 198, 722-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chair A;Reference number: S16022; MUID:91266957; PMID:2050149
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F.26-1528/Product: abrin-d chain B #status predicted <BCH>
F.261-528/Product: abrin-d chain B #status predicted <BCH>
F.261-528/Product: abrin-d chain B #status predicted <BCH>
F.283-325, 326-366, 369-407, 414-449, 413-429, 495-528/Region: 40-residue repeats
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F.1/A-113, 195, 196/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.200, 253, 361, 401, 402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.287-269, 286-305, 339-346, 417-430, 456-473/Pisulfide bonds: #status predicted
F.598, 312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 EQLAGNLRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QDQVIKFTTEGATSQSYKOFIEALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%; Score 327.5; DB 2; Length 528;
43.9%; Pred. No. 3.6e-22;
Live 22; Mismatches 68; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1562 <WOO>
A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-169,'C',171-320,'L',322-528 <HU2>
A;Cross-references: GB:M98346
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C;Species: Abrus precatorius (Indian licorice)
Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-
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nes 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: 1-72, V', 74-90, 'S', 92-233,'T', 235-267,'D', 269-289 <ZHE>
A; Molecule type: B: 370176; NID: 9547148; PIDN: AB31048.1; PID: 9547149
B; Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
B; Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
A; Biol. Chem. 265, 8665, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr
A; Reference number: A36273; MUID: 90256789; PMID: 2341399
                                                                                                                                                                                                                                                                                              A,Accession: A3623
A,Rolecule type: protein
A,Residues: 24-270 <COL>
R,Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A,Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A,Reference number: JT0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24 R.Xiong, J.P.; Xia, Z.X.; Wang, Y. Submitted to the Brookhaven Protein Data Bank, December 1994
A.Reference number: A66711; PDB:11CS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
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A;Residues: 24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL'
A;Experimental source: tuber
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submitted to the Brookhaven Protein Data Bank, July 1994
A;Reference number: A67091; PDB:1MKN
A;Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
K;Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A;Reference number: A67092; PDB:1MRK
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Nat. Struct. Biol. 1, 695-700, 1994

A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution
A;Reference number: A58622; MUID:95360714; PMID:7634073
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
C;Comment: Alpha-trichosanthin has been used to induce abortions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNKYTFAFGGNYDRLE 118
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10 INFITAGATVOSYTNFIRAVRGRLTVLPN----

72; Conservative

Matches

Query Match Best Local Similarity

A; Gene: tcs C;Genetics:

abrin-d precursor - Indian licorice (fragment) N; Contains: rRNA N-glycosidase (EC 3.2.2.22)

179 MRTRI 183 IGKRV 198

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Query Match
Best Local Similarity
Matches 72; Conserv
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A; Residues: 1-289 <MIZ>
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C; Superfamily: ricin; rRNA N-glycosidase homology
C; Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
F;35-286/Product: abrin-c chain A #status predicted <ACH>
F;41-280/Domain: rRNA N-glycosidase homology <RNG>
F;25-562/Product: abrin-c chain B #status predicted <BCH>
F;37-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F;377-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F;370-459,230/Buiding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;108,201/Active site: Glu, Arg #status predicted
F;108,201/Active site: Glu, Arg #status predicted
F;281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
F;281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
F;534,555/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Trichosanthes Xirilowii (Mongolian snake-gourd)
C;Species: Trichosanthes Xirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: JU0393; PS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin. A;Reference number: JU0393; WUID:92005921; PMID:1914000
A;Accession: JU0393
A;Note: a sequence which lacks Ala-247 is also shown in this publication A;Residues: 1-247 <TOY>
A;Note: a sequence which lacks Ala-247 is also shown in this publication C;Superfamily: TRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: abortifacient
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 327.5; DB 2; Length 562;
43.9%; Pred. No. 3.9e-22;
Live 22; Mismatches 68; Indels 15; Gaps
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Matches 82; Conservative
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C;Species: Trichosanthes kirilowii var. japonica
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 2.7-Reb-1997 #sequence_revision 27-Reb-1997 #text_change 23-May-1997
C;Accession: dG5032
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharman Bull. 19, 4455-1449, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka. A;Reference number: dG5032; MUID:97108848; PMID:8951169
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R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm Bull, 199, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka A;Reference number: JC5032; MUID:97108848; PMID:8951169
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**Residues: 22-270 eKON>
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-247_kKON>

C;Coment: This protein belongs to type I ribosomal-inactivating proteins which catalyti:
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
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N;Contains: karasurin A
C;Species: Trichosanthes Kirilowii var. japonica
C;Bate: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
C;Accession: JG5606; JG5033
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inacti
A;Reference number: JG5606; MUID:97386562; PMID:9212998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 326; DB 2;
39.6%; Pred. No. 2.3e-22;
tive 44; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 326; DB 2;
Pred. No. 1.9e-22;
karasurin-B - Trichosanthes kirilowii var. japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Mismatches
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Best Local Similarity 39.6%
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                 A;Accession: JC5032
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-247 <KON>
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173 RVGVSIRTN 181

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abrin-a precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text change 16-Jul-1999
C;Accession: S32429; JT0202; Ā39761; JC1398; S14472; S24Ī33; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Pitle: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A;Reference number: S32429; MUID:99132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                  R;Evensen, G.; Mathiesen, A.; Sundan, A.
Dalol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA A; Residues: 'M', 1-251 < EV2>
A; Residues: 'M', 1-251 < EV2>
A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Reywords: duplication; glycosidase; hydrolase; lectin; toxin
F; 7-225/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F; 7-246/Domain: rRNA N-glycosidase homology <RNS
F; 7-246/Domain: rRNA N-glycosidase homology <RNS
F; 7-4113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 164,167/Active site: Glu, Arg #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 61
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A;Note: the coding region for the sequence shown is preceded by an ATG codon A;Note: residues 1-8 were derived from the synthesized primer
A;Note: residues 1-8 were derived from the synthesized primer
A;Ruatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                    N.Contains: rRNA N-glycosidase (EC 3.2.2.2)
C.Species: Abrus precatorius (Indian licorice)
C.Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C.Accession: C39761; S14471
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R;Rvenen, G; Mathiesen, A.; Sundan, A.
R;Bvenen, G; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.0%; Score 310.5; DB 2; Length 251; Best Local Similarity 43.2%; Pred. No. 5e-21; Matches 79; Conservative 22; Mismatches 67; Indels 15
                                                                                                                                                                - Indian licorice (fragment)
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A, Residues: 'E', 2-528 <HUN>
                                                                                                                                                                abrin (clone 7.2) precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                             RESULT 10
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(Species: Abrus precatorius (Indian licorice)
(Species: Abrus precatorius (Indian licorice)
(Spacies: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
(Spacession: 832430; UC1399)
(R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
(Mol. Biol. 229, 263-257, 1993)
(A) Affille: Primary structure of three distinct isoabrins determined by cDNA sequencing. CC
A;Reference number: 832429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M98345; NID:g166296; PIDN:AAA32625.1; PID:g166297
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Bisci: Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422
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A;Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A;Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A;Experimental source: seed
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F;7-245/Domain: rRNA N-glycosidase homology cRNG>
F;7-245/Domain: rRNA N-glycosidase homology cRNG>
F;760-527/Product: abrin-b chain B #status experimental cBCH>
F;760-527/Product: abrin-b chain B #status experimental cBCH>
F;74,13,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;74,113,194,195/Binding site: substrate (Asn) (covalent) #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;266-269,265-304,328-345,416-429,455-472/pisulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                           142 GKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIOSTSEAARXKFIEDOIGK 196
                                                                                                                                                                                                                  63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                         GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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                                                  10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
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Best Local Similarity
Matches 83; Conserva
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A; Residues: 1-527 <HUN>
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C; Accession: JN0108
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A;Rolecule type: protein
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh
taining receptors on the cell surface. The A and B chains are linked by a single disulfi
C;Comperfamily: ricin; rRNA N-gjtyosidase homology
C;Reywords: duplication; gjtycosidase homology cRGP,
C;Reywords: duplication; gjtycosidase homology cRGP,
F;7-246/Domain: rRNA N-gjtycosidase homology cRGP,
F;7-246/Domain: rRNA N-gjtycosidase homology cRGP,
F;261-258/Product: abrin-a chain B #status experimental cBGP,
F;261-258/Product: abrin-a chain B #status experimental
F;263-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F;7/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
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A;Note: residues 1-8 were derived from the synthesized primer
A;Note: Lesidues 1-8 were derived from the synthesized primer
A;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biotchem. 57; 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1-201, 203-251 < FUN>
A; Residues: 1-201, 203-251 < FUN>
A; Residues: 1-201, 203-251 < FUN>
B; Bvensen, G; Mathiesen, A; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A; Fitle: Direct molecular cloning and expression of two distinct abrin A-chains.
A; Reference number: A39761; MUID:91201329; PMID:2016300
A; Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein frd
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Best Local Similarity 41.1%; Pred. No. 5.7e-20;
Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CHE>
B; Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.

Bur. J. Blochem. 240, 564-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110; MUID:97008945; PMID:8856055
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 'ME', 2-251 - EV2>
A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A;Title: The complete primary structure of abrin-a B chain.
A;Reference number: S24133; MUID:92371656; PMID:1505674
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A; Accession: JC1398
A; Accession: JC1398
A; Molecule type: protein
A; Molecule type: protein
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A;Nolecule type: DNA
A;Residues: 'E',2-251 <EVE>
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A;Molecule type: protein
A;Residues: 89-108;154-172 <LIN>
A;Experimental source: seed
A;Accession: S74111
                                                         A; Reference number: JT0202
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C; Species: Luffa cylindrica (smooth loofah)
C; Species: Luffa cylindrica (smooth loofah)
C; Apte: 17-Apt-1993 #sequence_revision 17-Apt-1993 #text_change 20-Aug-1999
C; Accession: S23519; S22113
R; Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 19, 887-889, 1992
A; Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating A; Reference number: S23519; MUID:92353400; PMID:1643290
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Agric. Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: JN0108; MUID:91248488; PMID:1368666
A;Accession: JN0108
                                                                                                                                                                                                                                                                   62 TLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
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138 AAGKVREKIPLGFRAFDSAITSLFHYDS----TAAAGAFLVIIQTTAEASRFKYIEGQI 192
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
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10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
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C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
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F;5-246/Domain: rRNA N-glycosidase homology <RNG>
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A;Molecule type: protein
A;Residues: 1-250 <ISL>
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Best Local Similarity
Matches 66; Conserv
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A; Residues: 1-278 < KAT>
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DB 2; Length 250;

30.2%; Score 293.5;

Query Match

QY 10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN	RESULT 15 RLPUGG rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor [validated] - balsam pear N;Alternate names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin alph C;Species: Momordica charantia (balsam pear, bitter gourd) C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 15-Sep-2000 C;Accession: S14273; A61318; S16490; JN0628; S01670 R;Ho, W.K.K.; Liu, S.C.; Shaw, P.C.; Yeung, H.W.; Ng, T.B.; Chan, W.Y. Bjochim. Biophys. Acta 1088, 311-314, 1991 A;Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein. A;Reference number: S14273; MUID:91159486; PMID:2001404	A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> A; Residues: 1-286 <how> R; Li, S.S.L. Experientia 36, 524-527, 1980 A; Title: Purification and partial characterization of two lectins from Momordica charantial A; Reference number: A61318; MUID: 80201763; PMID: 7379938 A; Accession: A61318 A; Molecule type: protein A; Redidues: 24-50 <lia> A; Molecule type: protein A; Redidues: 24-50 <lia> A; Note: as a lectin shows agglutinating activity for type-O red blood cells A; Note: as a lectin shows agglutinating activity for type-O red blood cells A; Note: B; R; Montecucchi P; C; Lazzarini, A.M.; Barbieri, L.; Stirpe, F.; Soria, M.; Lappi, D. Int., V; Pept. Protein Res. 33, 263-267, 1889 A; Title: N-terminal sequence of some ribosome-inactivating proteins. A; Reference number: S16331; MUID: 89326691; PMID: 2753596</lia></lia></how></how></how></how></how></how></how></how>	A;Accession: S16490 A;Rocassion: S16490 A;Rocassion: S16400 A;Rosidues: 24-68, X',70 cMON> R;Minami, Y', Funatusu, G' B;Diamai, Y', Funatusu, G' B;Diamai, Y', Funatusu, G' B;Diosci. Biotechnol. Biochem. 57, 1141-1144, 1993 A;Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating protein A;Reference number: UN0628; MUID:93372485; PMID:7763984 A;Accession: UN0628 A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Experimental source: seed R;Ren, J', Wang, Y', Dong, Y', Stuart, D.I. Submitted to the Brockhaven Protein Data Bank, January 1994 A;Reference number: A52272; PDR:1AHC	A; Concents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-269 R; Humain, J.; Tickle, I.J.; Wood, S.P. S; Bilmasin, J.; Tickle, I.J.; Wood, S.P. S; Humain, J.; Tickle, I.J.; Wood, S.P. A; Reference number: A52385; PDB:1MOM A; Contents: annotation; X-ray crystallography, 2.16 angstroms, residues 24-86, L', 88-269 R; Humang, O.; Liu, S.; Tang, Y.; Jin, S.; Mang, Y. S; Humang, O.; Liu, S.; Tang, Y.; Jin, S.; Mang, Y. S; Humang, O.; Liu, S.; Tang, V.; Jin, S.; Mang, Y. A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, R', 79-132,' A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, R', 79-132,' C; Function: A; Description: hydrolyzes rRNA N-glycosidase; nonlogy C; Superfamily: RNA N-glycosidase; rRNA N-glycosidase; lectin; seed; toxin F;1-18/Domain: signal sequence #status predicted <pro> F;19-23/Domain: amino-terminal propeptide #status predicted <pro></pro></pro>
Best Local Similarity 33.7%; Pred. No. 1.8e-19; Matches 63; Conservative 46; Mismatches 57; Indels 21; Gaps 4; Qy 10 INFTAGATVQSYTNFIRAVEGLTVLPNRVGLDFINQRFILVELSNHAEL 59 S:	uffin-A	protein from	ein from -209,'SL'	drolyzes the N-19 consider of a specific adenosine in 285 rRNA ther drolyzes the N-19 cosidase; rRNA N-19 cosidase; rRNA N-19 cosidase; rRNA N-19 cosidase; rRNA N-19 cosidase; rRNA N-19 cosidase; rand N-19 cosidase; rand N-19 cosidase alpha-luffin #status experimental <pre></pre>

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F;24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>F;27-266/Domain: rRNA N-glycosidase homology <RNG>F;270-286/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;370-286/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;33,183,186/Active site: Tyr, Glu, Arg #status predicted F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Query Ma	tch al cim	بنبورب	28.18;	Score	273; D	17;	Length ;	1987			
Described 3; Conservative 40; Mismatches 62; Indels 16; Gaps 4;	63;	Conserva	stive 4	o, Mi	smatches	62;	Indel	3 16;	Gaps	4;	
ζ,	10 IN	FTTAGATV(10 INFITAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSVT 62 :: : : : :	VRGRLT:	VLPNRVGL :	PII	NORF	ILVELSNE	ARLSVT	62	

⁸⁵ VAVDVINVYIMGYLADTISYFF---NEPAAELASQYVFRDARRKIILPYSGNYERLQIAA 141 셤

ð 원

à 엄

¹⁸² R 182 197 R 197

Search completed: February 10, 2004, 16:28:01 Job time : 10.2276 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:13:55; Search time 6.30467 Seconds (without alignments) 1409.756 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-083-336A-6 971 1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 189

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

		Description	9 ricinus c	P06750 ricinus com	P09989 trichosanth	P28590 abrus preca	_	Q06077 abrus preca		P33183 sambucus ni	ß	abrus	luffa	cucumi	Q00465 luffa cylin		•	'n	ın	P33186 gelonium mu		P21326 mirabilis j	phytolacca		31			٥	27559		P04399 hordeum vul	P27560 saponaria o	15 bacterio	4	5
SUMMARIES	;	ai .	뒨	AGGL_RICCO	RIPT TRIKI	ABRC ABRPR	RIPS TRIKI	ABRB ABRPR	RIP2_BRYDI	NIGB SAMNI	RIP1 BRYDI	ABRA ABRPR	RIPB_LUFCY	RIP1 CUCFI	RIPA_LUFCY	RIP1 MOMCH	RIP2 MOMBA	MLA VISAL	RIPI TRIAN	RIPG GELMU	RIPA PHYAM	RIPP_MIRJA	RIP1_PHYAM	RIPS PHYAM		RIPS SAPOF	RIP2 PHYAM	RIP6 SAPOF	RIP2_SAPOF	RIPO DIACA		RIP3 SAPOF			RIDS MATZE
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	į	Score	95	861.5	336	327.5	326	323	320.5	307.5	305	303.5	293.5	281.5	274.5	273	272	264	257	243.5	186.5	174	170	168.5	131	127	125	124	121	116.5	114	110	108		103.5
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RIPX MAIZE RIP9_MAIZE RIP9_MAIZE SLTA_BPH19 SLTA_BPH30 SYV_AQUAE J16 HORVU Y348_MYCPN ORPB_HUMAN ORPB_HUMAN RIP4_SAPOF RIP4_SAPOF ORPW_VIBER GPH_HAEIN
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101.5 97 95 94 85.5 81.5 76.5 76.5 76.5
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ALIGNMENTS

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specific adenosine on the 28S TRNA.
SUBUNIT: Disulfide-linked dimer of A and B chains.
DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                  recombinant ricin A-chain at 1.8-A resolution.";
                                               MEDIINE=87165983; Pubmed=3558397; Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Montent W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Wuterber E., Kuong N.E., Hamlin R., Robertus J.D.; "The three-dimensional structure of ricin at 2.8 A."; J. Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
MEDLINE=96374222; PubMed=8780513;
DAY P.J., Enrat S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svinth M.C., Robertus J.D.;
"Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
MEDILINE-25082010; Pubmed=7990130;
MESTON S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
Paupcit R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. WEDLINE=91352005; PubMed=1881882; Rutenber E., Robertus J.D.; Rutenber E., Robertus J.D.; Richard G. Richall B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN
                                                                                                                                                          MEDLINE=91352004; PubMed=1881881;
Katzin B.J., Collins E.J., Robertus J.D.;
"Structure of ricin A-chain at 2.5 A.";
                                           X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3iochemistry 35:11098-11103(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93165632; PubMed=1287657;
                                                                                                                                                                                                                                                                                                                                                                                             J. Mol. Biol. 244:410-422(1994).
             Toxicon 39:1723-1728(2001).
                                                                                                                                                                                                     Proteins 10:251-259(1991)
                                                                                                                                                                                                                                                                                                                                                                                  'X-ray structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robertus J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGENESIS
 "Ricin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 11L4; 16-JAN-02.

R PDB; 11L9; 16-JAN-02.

R GlycosuiteDB; POSST9; --.

R InterPro; IPR001572; Ricin_B_lectin.

R InterPro; IPR001574; RIP.

R Pfan, PPR00652; Ricin_B_lectin, 6.

R Pfan, PPR00652; RIGARICIN.

SMART; SM00458; RICIN, 2.

R PROSITE; PS00275; SHIGARICIN, 1.

R PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN, 1.

PROSITE; PS00275; SHIGARICIN; 1.
SIMILARITY: Contains 2 ricin B-type lectin domains.

GUJTON: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).

DATABASE: NAME=Protein Spotlight;

NOTE=1ssue 31 of February 2003;

WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
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N-LINKED (GLCNAC. .) (IN MINOR FORM).

N-LINKED (GLCNAC. .).

N-LINKED GLCNAC. .).

E -> D (IN REF. 3).

A -> R (IN REF. 3).
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LINKER PEPTIDE.
RICIN B CHAIN.
RICIN B-TYPE LECTIN 1.
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1APG; 31-JAN-94.
1FMP; 31-OCT-93.
1IFS; 14-JAN-98.
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1BR6; 02-SEP-98.
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                                                                                                                                                                                   96 BLSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFG 155
                                                                                                                                                          52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                         112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                  156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                  36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agglutinins from Ricinus communis.";

Bur. J. Biochem. 105:453-459(1980).
-!- CATALYTY CACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the SES TRNA.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOWE-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (RC 3.2.2.2); Agglutinin B chain].
Ricinus communis (Castor bean)
Ricinus communis (Lastor bean)
Ricinus communis (Sastor bean)
Robernatophyta; Hadnotiophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Malpighiales; Euphorbiacee; Ricinus.
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                                                                             2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINORFILV
                                           Gaps
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                                       0; Indels 10;
Score 951; DB 1; Length 576;
Pred. No. 3.2e-80;
0; Mismatches 0; Indels
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Lin T.T.-S., Li S.S.-L.;
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  97.9%;
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EMBL; M12089; AAA33869.1; -. EMBL; S40368; AAB22584.1; -.

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               HSSP, P02879; IBR6.

GlycosniteDB; P06750; -.

InterPro; IPR001574; Rich B_lectin.

Ffam; PR0052; Rich B_lectin; 6.

Pfam; PR0052; Rich B_lectin; 6.

Pfam; PR00156; RHGARICIN.

SMART; SM00458; RICIN; 2.

PROSITE; PS00231; RICIN; 2.

PROSITE; PS00231; RICIN B_LECTIN; 2.

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01-NOV-1990 (Rel. 16, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor (RRNA N-glycosidase) (EC 3.2.2.2) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
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X.-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
MEDLINE=94344957; PubMed=8066085;
Abou F., Pu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
Proteins 19:4-13(1994).
                                                                                                     SEQUENCE OF 24-270.
STRAIN=Maximowicz; TISSUE=Tuberous root;
MEDLINE=90256789; PubMed=2341399;
                                                                                                                                                                              Pure Appl. Chem. 58:789-798(1986).
                                                                   STRAIN=Maximowicz; TISSUE=Leaf;
MEDLINE=90256790; PubMed=2341400;
                                                    Gene 97:267-272(1991)
                                                           [2]
SEQUENCE FROM N.A.
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PDB; 1QD2; 24-APR-00.

PLGEATO; 1PR01574; RIP.

Pfam; PF00161; RIP; 1.

PRINTS; PR00396; SHIGARICIN.

PROSITE; PS00275; SHIGA RICIN; 1.

PROSITE; PS00275; SHIGA RICIN; 1.

PROSITE; PS00275; SHIGA FICIN; 1.

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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its modified anothris is such that so content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-270.

TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Mi C.Z.;
"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";
                                                                                                                                                                                                                               Chow T., Feldman R.A., Lovett M., Piatak M.;
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"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
J. Biol. Chem. 265:8665-8669(1990).
                                                                            SEQUENCE FROM N.A.
STRAIN=Maximowicz;
STRAIN=B1153657;
Strain W.K.K., Ng T.B., Yeung H.W.;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M34858; AAA34207.1; -. EMBL; J05434; AAA34206.1; -.
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Gaps
RIBOSOME-INACTIVATING PROTEIN ALPHA-
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                                                                                     | PLL -> LDLI (IN REF. 4).
| MISSING (IN REF. 4).
| MISSING (IN REF. 4).
| V -> VDAGLDENRAYL (IN REF. 4).
| X -> GL (IN REF. 4).
| X -> GL (IN REF. 4).
| WS -> LML (IN REF. 4).
| WS -> LML (IN REF. 4).
| WS -> LML (IN REF. 4).
| WS -> LML (IN REF. 5).
| WS -> MISSING (IN REF. 2).
| MISSING (IN REF. 2).
| MISSING (IN REF. 2).
| T -> M (IN REF. 2).
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38.9%; Pred. No. 7.9e-24;
Live 42; Mismatches 49; Indels
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                         TRICHOSANTHIN.
MISSING IN MATURE PROTEIN.
BY SIMILARITY.
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Best Local Similarity
Matches 72; Conserv
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. JT0566; RLTZT. 1 MRJ, 07-FEB-95. 1 MRK, 07-FEB-95. 1 TCS; 10-JUL-95. 1 JJG; 28-JAN-03.

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us-10-083-336a-6.rsp

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Mood K.A., Lord J.M., Wawrzynzak E.J., Piatak M.;

Wood K.A., Lord J.M., Wawrzynzak E.J., Piatak M.;

"Preproabrin: genomic clouhing, characterisation and the expression of the A-chain in Escherichia coli.";

Eur. J. Biochem. 198:733-732 (1991).

STYTHESIS THROUGH THE CATALYTIC INCCTIVATION OF 60S RIBOSOMAL STRUCHESIS THROUGH THE CATALYTIC INCCTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SRNA. THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE AND ECHAINS.

CHAIN IS A CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

CHAIN THE B CHAIN IS COMPOSED OF TWO DOWAINS, EACH DOMAIN CONSISTS OF 3 HOWOLGOUS SUBDOWAINS, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CHAIN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                      82 TISVALDVTNVYIMGYRAGDISYFF---NEASATEAAKXVFKDAMRKVTLPYSGNYERLQ 138
                                                              SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLE 118
                                                                                                                             119 OLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGE 178
                                                                                                                                              25 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLIRSSLFGSQRYALIHLINYADE 81
                                                                                                                                                                                                                                                                                                                       P28590;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 1, Last amnotation update)
Abrin-c precursor (Contains: Abrin-c A chain (rRNA N-glycosidase)
(EC 3.2.2.2); Abrin-c B chain].
(EC 3.2.2.2); Abrin-c B chain].
EURATYOCA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 10 INFTTAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINORFILVELSNHAEL
                                                                                                                                                                                                                                                                                                             562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11140; 1ABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00165; Ricin_B_lectin; 6.
Pfam; PF00161; RIP, I.
PRINTS; PR001396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91266957; PubMed=2050149;
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                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                179 MRTRI 183
                                                                                                                                                                                                                              194 IGKRV 198
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118 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97356562; PubMed=9212998; Mizukami H., Iida K., Kondo T., Golhara Y.; Mizukami H., Iida K., Kondo T., Colhor and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 ODQVIKETTEGATSQSYKQFİEALRQRLİGGLIHDIPVLPDPTTVEERNRYİTVELSNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core eudicots; Rosidae;
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                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCKAC. . ) (POTENTIAL).
N-LINKED (GLCKAC. . ) (POTENTIAL).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
              BY SIMILARITY.
ABRIN C A CHAIN (BY SIMILARITY).
LINKER PEPTIDE (BY SIMILARITY).
ABRIN C B CHAIN (BY SIMILARITY).
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
1-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            33.7%; Score 327.5; DB 1; Length 562;
Pyrrolidone carboxylic acid
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.22).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                 62817 MW; 1FD0ABC7D7BA6278 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.9%; Pred. mo.
tive 22; Mismatches
                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                   2-ALPHA.
2-BETA.
                                                                                                                                                     1-GAMMA.
                                                                                                                                   1-BETA.
                                                                                                                                                                                                      2-GAMMA
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Biol. Pharm. Bull. 20:711-713(1997)
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SEQUENCE OF 24-270.
MEDLINE=92005921; PubMed=1914000;
Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82; Conservative
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3303
3339
380
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295
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435
462 AA;
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TISSUE=Root tuber;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3677;
   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIKI
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DISULFID
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                                  CHAIN
PEPTIDE
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REPEAT
REPEAT
                                                                                 DOMAIN
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REPEAT
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                   SIGNAL
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                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 INFTTAGATVQSYTNFIRAVR----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                       Chem. Pharm. Bull. 39:1244-1249(1991).
-!- FUNCTION: ABORITON-INDUCING PROTEIN. IT INACTIVATES EUKARXOTIC
-|- FUNCTION: SUBENITS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  006077; P81374;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(RC 3.2.2.2); Abrin-b B chain].
(RC 3.v. viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Mismatches 50; Indels 16; Gaps
                                                                                                                                                                                                                       specific adenosine on the 28S FRMA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB000666; BAA21786.1; -.
PIR, JC5606, JC5606.
PIR, JU0393; JU0393.
HSSP; P09999; IMMJ.
InterPro; IPR001574; RIP.
Pfam, PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
PRINTS; PR00375; SHIGARICIN; 1.
PRINTS; PR00375; SHIGARICIN; 1.
PRINTS; PR00375; Protein synthesis inhibitor; Hydrolase;
                                     "The complete amino acid sequence of an abortifacient protein,
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.6%; Score 326; DB 1; Length 289; 39.6%; Pred. No. 6.6e-23;
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BY SIMILARITY.
883D3E3242887B26 CRC64;
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24 270 KA
271 289 RE
183 183 BY
289 AA; 31704 MW;
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270
289
183
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                                                               karasurin."
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ACT_SITE
SEQUENCE
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abrin-b, coxic proteins from the seeds of Abrus precatorius.",
Blosci. Biotechnol. Biochem. 57:166-169(1993).

-!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
ABRIN-A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
RACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
PRECEDES ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S TRNA.

-!- SUBUNIT: DISULFIDE-LINKED DIMER OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

-!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; Proved; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SWART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B. LECTIN; 2.
PROSITE; PS50275; SHIGA-TICIN; 1.
PROSITE; PS50275; SHIGA-TICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; dlycoprotein; Lectin; Pyrrolidone carboxylic acid.

1 250 ABRIN-B A CHAIN.
1 250 ABRIN-B A CHAIN.
1 LINKER PEPTIDE.
1 LINKER PEPTIDE.
                                                                                                                                MEDLINE=93169023; PubMed=7763422;
Kimura M., Sumizawa T., Funatsu G.;
"The complete amino acid sequences of the B-chains of abrin-a and
                Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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INTERCHAIN (BY SIMILARITY).
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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2-BETA.
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HSSP, P11140; JABR.
InferPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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MEDLINE=93132798; PubMed=8421313;
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                                                                                                SEQUENCE OF 260-527.
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58 ELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
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D -> N (IN REF. 2).

AE -> PQ (IN REF. 2).

L -> M (IN REF. 2).

Y -> D (IN REF. 2).

Y -> D (IN REF. 2).

N -> S (IN REF. 2).

N -> S (IN REF. 2).

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N -> S (IN REF. 2).

H -> Y (IN REF. 2).

E -> Q (IN REF. 2).

H -> Y (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).
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21; Mismatches
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43.9%;
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Eukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Bryonia. PRT: 282 AA.
P98184; Q9S8JO;
P08184; Q9SSJO;
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
glycosidase) (EC 3.2.2.2) (BD2).
Bryonia dioica (Red bryony). NCBI_TaxID=3652; RESULT 7

Siegall C.B., Gawlak S.L., Marquardt H., "Bryodin 2 a ribosome-inactivating protein isolated from the plant Patent number US5597569, 28-JAN-1997 SEQUENCE FROM N.A. Bryonia dioica.";

MEDLINE=95151812; PubMed=7849072; SEQUENCE OF 22-42.

Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;

"Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates.";

Bioconj. Chem. 5:423-429(1994).
-!- PUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at or specific adenosine on the 28S RNN.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.

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N-LINKED (GLCNAC. .) (POTENTIAL).
C52BE2F6A873769C CRC64; InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00196; SHIGARICIN.
PROSTIE; PS00275; SHIGARICIN:
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; 563 AA Multigene family; Glycoprotein; Signal. PRT; EMBL; 134238; -; NOT_ANNOTATED_CDS. HSSP; P09989; 1MRJ. 183 183 B 25 25 N 282 AA; 30754 MW; 81; Conservative STANDARD: P33183; P33184; P93542; 282 183 Local Similarity P09989 NIGB SAMNI ACT SITE CARBOHYD SEQUENCE Query Match CHAIN This Matches 셤 g à ò à

Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra)."; 01-0CT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
38-FEB-2003 (Rel. 41, Last sequence MEDINE-94003077; PubMed-8400135;
RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
RA, Munoz R., Arias F.J., Calonge M., Gazcia J.R., Mendez E.;
RT Isolation and partial characterization of nigrin b, a non-toxic
RT novel type 2 ribosome-inactivating protein from the bark of Sambucus
RT nigra L.",
Plant Mol. Biol. 22:1181-1186(1993)
CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN nigra L."; Plant Mol. Biol. 22:1181-1186 (1993). -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN Eur. J. Biochem. 237:505-513(1996). MEDLINE=96215449; PubMed=8647092; SEQUENCE OF 26-49 AND 298-321. TISSUE=Bark; SEQUENCE FROM N.A. NCBI_TaxID=4202;

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C.B.;
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      SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBDINITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                        CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
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PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS50231; RICIN_B LECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific adenosine on the 28S rRNA.
SUBUNIT: DISULFIDE-LINKED DINER OF A AND B CHAINS.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
SIMILARITY: Contains 2 ricin B-type lectin domains.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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PIR; S37382; S37382.
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Best Local Similarity 38.2.
The 73; Conservative
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---SVARSLLVVIQMVSEAARFRY 194
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-i- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS.
-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
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F13185; 095819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
-2.2.22) (BD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL PRODUCE A SHORTER PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97228081; PubMed-9115985;
Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N^terminal sequence of some ribosome-inactivating proteins."; Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bryonia dioica and their utility as carcinoma-reactive
142 DNLETAANTRRESIELGPSPLDGAITSLYHGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent number US5541110, 30-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89326691; PubMed=2753596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bryonia dioica.";
Biochemistry 36:3095-3103(1997).
                                                                             175 IEGEMRTRIR 184
                                                                                                                                                       195 İEQEVRRSLQ 204
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142 GKIRENIPLGLPALDSAITTLYYYTAS-----SAASALLVLIQSTAESARYKFIEQQIGK 196 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181

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RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN. BY SIMILARITY.
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35.7%; Pred. No. 5.8e-21;
Live 45; Mismatches 56; Indels 16; Gaps
                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
E-K. REDUCES ACTIVITY 10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                                            PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                    31788 MW; E966CD9C031A42DB CRC64;
                                                                 D-structure; Multigene family; Glycoprotein; Signal
an email to license@isb-sib.ch)
           EMBL; 124020; -; NOT_ANNOTATED_CDS
PIR; S16491; S16491.
                         PDB; 1BRY; 04-MAR-98.
InterPro; 1PR001574; RIP.
Pfam; PF00161; RIP; 1.
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63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121

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INFTTAGATVOSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT 25 VSFRLSGATTTSYGVFIKNIREALPYERKVYNIPLIRSSISGSGRYTLLHLTNYADETIS

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TABLIANCE STATEMENT (2.1.7 AND STATEMENT)

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TABLIANCY T.H., LU T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin structure of constructure of constructure of abrin structure of constructure      P11140; P28589; Created)
01-JUL-1989 (Rel. 1), Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Abrus precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
(EC 3.2.1.22); Abrin-a B chain].
Abrus precarcivis (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicuts; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=93132798; PubMed=8421313;

Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
The complete primary structure of abrin-a B chain.";
FEBS Lett. 309:115-118(1992).
528 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91201329; PubMed=2016300;
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STANDARD;
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DR Pfan; PRO035; RICH B. lectin.
DR Pfan; PRO035; RICH B. lectin.
DR PRATT; SM00458; RICHN:
DR SWART; SM00458; RICHN:
DR SWART; PRO035; SHIGARICH:
PROSITE; PRO027; Protein synthesis inhibitor; Toxin; Repeat;
PROSITE; PRO027; Protein synthesis inhibitor; Toxin; Repeat;

"Aut defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
"Aut defense; Hydrolase; Protein synthesis inhibitor;
"S25 261 LINKER PEPTIDE.
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"G25 261 LINKER PEPTIDE.
"G27 RICHN B-TYPE LECTIN 1.
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INTERCHAIN (BY SIMILARITY).
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N-LINKED (GLCNAC...).
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   INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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Gaps

10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 61

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RESULT 13
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                              62 TLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ 119
                                                                           120 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                         60 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 INFTTAGATVQSYTNFIRAVRGRL------TVLPNRVGLPINQRFILVELSNHAEL 59
         64
                                                                                                                                                                                                                                                                                                                                                                                             Islam M.R., Hirayama H., Funatsu G.;

"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";

Agric. Biol. Chem. 55:229-8(1991).

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                       (EG 3.2.2.22).

Luffa cylindrica (Smooth loofah) (Sponge gourd).

Luffa cylindrica (Smooth loofah) (Sponge gourd).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%; Score 293.5; DB 1; Length 250; 33.7%; Pred. No. 5.6e-20; trive 46; Mismatches 57; Indels 21.
                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AA; 27293 MW; F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                         250 AA.
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91248488; PubMed=1368666;
                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 RTRIRYN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 IERIPKN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JN0108; JN0108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                176 RVSIQ 180
                                                                                                                          180 RTRIR 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Yamada T., Ohki S.T., Osaki T.;

Yamada T., Ohki S.T., Osaki T.;

"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";

Plant Blotechnol. 17:337-340(2000).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 NLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSNHAELSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 VKFSLLGSNHKSYSKFITSMRNALPNAGDIYNIPLLVPSISGSRRYILMQLSNYEGNTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 MAVDVINVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQSVAR
                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                           Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00161; RIP, 1.

BRNTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
Plant defense; AntivixaI; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 286;
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103 103 N-LINKED (GLCNAC. .) (PO

110 110 N-LINKED (GLCNAC. .) (PO

252 252 N-LINKED (GLCNAC. .) (PO

265 AA; 31771 MW; 4EFD4966E604DA41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%; Score 281.5; DB 1 32.4%; Pred. No. 8.4e-19;
                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Mismatches
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB045560; BAB19677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
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  STANDARD;
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286
185
103
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252
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                                                                                                                                                                                                Cucumis figarei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
RIP1 CUCFI
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 KAITVAVDVTNVYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYEKLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 QLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 VRFSLSGSSSTSYSKFIGDLR---KALPSN-GTVYNITLLLSSASGASRYTLMTLSNYDG 77
                                                                                                                                                                                                                                                                                                                             inactivating protein from Luffa cylindrica.";
Plant Mol. Biol. 18:1199-1202(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 INFTTAGATVOSYTNFIRAVRGRLTVLPNRVGLPIN------QRFILVELSNHAE
                                                                                                                            N-g_rYcosidase, (EC 5.2.2.21.
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIBOSOME-INACTIVATING PROTEIN LUFFIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfan; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                               Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 277;
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                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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              277 AA.
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InterPro; IPR001574; RIP.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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--- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
--- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                      01-APR-1990 (Rel. 14, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-SR-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momoratin I precursor (rRNA
N-glycosidase) (EC 3.2.2.22) (Alpha-momorcharin) (Alpha-MMC).
Momordica charantia (Bitter gourd) (Balsam pear).
Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=91159486; PubMed=2001404;
Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;
"Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casellas P., Dussossoy D., Falasca A.I., Barbieri L., Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F.; "Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii Maximowicz. Purification, partial characterization and use for preparation of immunotoxins."; Eur. J. Biochem. 176:581-588(1988).
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MEDLINE=94356447; PubMed=8075985;
Ren J., Wang Y., Dong Y., Stuart D.I.;
The N-glycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of alpha-momorcharin.";
Structure 2:7-16(1994).
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Husain J., Tickle I.J., Wood S.P.;
"Crystal structure of momordin, a type I ribosome inactivating
protein from the seeds of Momordica charantia.";
PEBS Lett. 342:154-158(1994).
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Int. J. Pept. Protein Res. 33:263-267(1989).
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Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
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PROSITE; PS00275; SHIGA RICIN.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Signal; Glycoprotein; 3D-structure.
SIGNAL
                                                                                                    RIBOSOME-INACTIVATING PROTEIN MOMORDIN I. MISSING IN MATURE PROTEIN.
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Pfam; PF00161; RIP; 1.
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Ortigao M., Better M.;
Ortigao M., Better M.;
Ortigao M., Better M.;
'Momordin II, a ribosome inactivating protein from Momordica
balsamina, is howologous to other plant proteins.";
Nucleic Acids Res. 20.4662-4662(1992).
-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
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Momordica balsamina (Bitter gourd) (Balsam pear).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
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141 KIRBNIDLGLPALSSAITTLFYYNA----QSAPSALLVLIQTTAEAARFKYIERHVAKY 195 ДQ

183 IRYN 186

à

: | : 196 VATN 199

q

Search completed: February 10, 2004, 16:23:24 Job time : 7.30467 secs

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February 10, 2004, 16:17:00; Search time 25.2187 Seconds (without alignments) 1933.961 Million cell updates/sec
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1 MIFPKQYPIINFTTAGATVQ.....ARFQXIBGEMRTRIRYNRRS 189
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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1: Sp_archea:*
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5: sp_tung:*
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5: sp_manmal:*
5: sp_mhc:*
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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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sp_virus:*
sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q41174 ricinus com	Q94bw3 cinnamomum	Q94bw4 cinnamomum	Q94bw5 cinnamomum	Q9fv22 cinnamomum	Q94ke4 trichosanth	Q41216 trichosanth	004367 sambucus ni	.Q9lre3 trichosanth	Q9avr2 sambucus eb		Q8lpv7 trichosanth		Q945s2 sambucus ni	Q8gt32 sambucus ni	Q41611 trichosanth
SUMMARIES		; ; ;																
SOM		TD CT	041174	Q94BW3	Q94BW4	Q94BW5	Q9FV22	Q94KE4	041216	004367	Q9LRE3	Q9AVR2	006076	Q8LPV7	038760	094552	Q8GT32	041611
			10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
		Match Length DB	541	580	580	581	549	289	289	563	247	564	528	270	252	563	563	270
,	* Query	Match I	97.9	38.6	38.4	38.2	38.0	34.4	34.2	33.9	33.6	33.3	32.8	32.6	32.0	31.7	31.7	31.4
		Score	951	374.5	372.5	370.5	368.5	334	332	329.5	326	323.5	318.5	317	310.5	307.5	307.5	305
	Result	No.	н	7	e	4	S	9	7	80	Q	10	11	12	13	14	15	16

541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;

24 29.73 28.1 264 10 09F632 09F6812 09F6812 00F6812 00F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F6812 00 09F682 00 09	1 41174 PRELIMINARY; P	ALIGNMENTS	5 245.5 25.3 603 10 Q9M653 Q9m653	246.5 25.4 275 10 Q8H1Y4 Q8h1y4	246.5 25.4 203 10 QBRY69 QBRY69	247 25.4 293 10 Q8VYU0 Q8vyu0	247 25.4 258 10 Q9S9E4 Q9s9e4	251 25.8 249 10 08RXH7 OBrxh7	253 26.1 531 10 OBRXH6 OBRXH6 AL	259 26.7 293 10 Q8S452 Q88452 jatropha	259 26.7 251 10 QBLKQ4 QBLKQ4 viscum al	260 26.8 573 10 Q8W2E8 Q8w2e8	260 26.8 254 10 Q8LKQ6 Q8lkq6	263 27.1 565 10 Q8W243 Q8w243	265 27.3 286 10 Q41257 Q41257 momordica	266.5 27.4 604 10 Q9M654 Q9m654	27.5 570 10 022415 022415 022415 sambucus n	270 27.8 249 10 QBLKQ5 QBLKQ5 270 27 R 286 10 OGFRW7 OGFRW7	271 27.9 592 10 Q8W2E7 Q8w2e7	273 28.1 570 10 Q41358 Q41358	273 28.1 264 10 Q9FSH2 Q9fsh2	250.55 29.9 T TO 0362.35	293.5 30.2 566 IO 004072 004072	296.5 30.5 251 10 Q96237 Q96237 Q96237 30.2 566 10 Q06072 Q064072 Q064072 Q064072 Q067	297.5 30.6 251 10 Q96236 Q96236 296.5 30.5 251 10 Q96237 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q96227 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627 Q9627	298.5 30.7 547 10 Q9M6E9 Q9mee9 abrus 297.5 30.6 251 10 Q96236 Q96236 Q96237 abrus 296.5 30.2 251 10 Q96237 Q96237 abrus 293.5 30.2 566 10 Q06072 Q06072 abrus 200.5 30.2 566 10 Q06072 Q06072 Abrus	300.5 30.9 278 10 000980 000980 298.5 30.7 547 10 090689 00980 096236 296.5 30.6 251 10 096236 096236 096236 296.5 30.5 251 10 096236 096236 096236 096236 096236 096236 096236 096236 096237 096227 096227 096227 096227 096227 096227 09627 09		WENTS 541 AA.	0.55.55.50 0.41358 0.41358 0.6180257 0.22415 0.62415 0.61804 0		261 261 262 263 265 270 604 251 251 253 253 253 253 253 253 253 253 253 253	7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2013 2013 2013 2014 2014 2015 2015 2016 2016 2016 2016 2016 2016 2016 2016	RESCULT 5 4 4 4 4 2 2 4 5 4 5 4 5 4 5 4 5 4 5 6 4 6 4 6 4 6 4
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SEQUENCE FROM N.A. MEDLINE=92338377; PubMed=1633311; MEDLINE=92338377; PubMed=1633311; MODCHIS L.M., Tregear J.W., Lord J.M.; "Molocular cloning of ricin." Targeted Diagn. Ther. 7:81-97(1992). -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SIMILARITY: BELONGS TO THE 28S RRNA. -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; \$40366, AAR22582.1; -. HSSP; P02879; IBR6. Ricinus communis (Castor bean). Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus. U411/4; UAVOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NAR-2003 (TrEMBLrel. 23, Last annotation update) Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase) InterPro; IPR00172; Ricin_B_lectin. InterPro; IPR001574; RIP. InterPro; IPR001574; RIP. InterPro; IPR001400; Somatotropin. Pfam; PF00161; RIP; I. PRINTS; PR00196; SHIGARICIN. SMART; SW00458; RICIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS00275; SHIGA_RICIN; 1. NCBI_TaxID=3988; (Fragment).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                 121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                            GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 YPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSN-H 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 YQTVTFTTKNATKISYTQFIEALRAQLASGEEPHGIPVWRERSTVPDSKRFILVELSNWA 92
                                                                          2 IFPKQYPIINPTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 51
                                                                                                           1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patterns.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                        10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIFIC ADENOSINE ON THE 288 RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AV039803; AAR82460.1; -.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
17pe 2 ribosome-inactivating protein cinnamomin III precursor (EC 3.2.2.2) (rRNA N-91ycosidase).
   Length 541;
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580 AA; 64421 MW; 940D10F01E7FB558 CRC64;
 97.9%; Score 951; DB 10;
94.9%; Pred. No. 2.8e-82;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.6%; Score 374.5; DB 1
48.1%; Pred. No. 3.7e-27;
tive 26; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CINNAMOMIN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGARICIN.
SMART; SMO458; RICIN; 2.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cinnamomum camphora (Camphor tree)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                    172 FOYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                       181 FOYIEGEMRTRIRYNRRS 198
                                       Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 ADSPVALAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYTD 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSN-H 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRDGSTVPDSKRFILVELSNWA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDDGLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AND9802; AAK8A59-1; -.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y., Yang O., Gong Z.Z., Liu W.Y., Wolecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 38.4%; Score 372.5; DB 10; Length 580;
Local Similarity 47.6%; Pred. No. 5.8e-27;
les 89; Conservative 27; Mismatches 56; Indels 15; Gaps
                                                                                                                                                                                                                                                     Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                 Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR-2003 (TrEMBLrel. 2), Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CINNAMOMIN II.
37E4289ECCE0CBFF CRC64;
                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                           580 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00396; SHIGARICIN.
SWART; SMOAFS, RICIN; 2.
PROSITE; PS5021; RICIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 580 AA; 64265 MW;
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                                                                                                                           PRELIMINARY;
                                  208 YRVRESI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 GEMRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 YRVRESI 214
177 GEMRTRI 183
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                       patterns.
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                                                                                                                                            Q94BW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94BW5
                                                                                                                           094BW4
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InterPro; IPR000772; Ricin_B_lectin.
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Signal; Toxin.
                     InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                      90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 YRVRGSI 182
                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                         Hydrolase; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 ADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PALENLLPDTK-RYTFPFSGSYTD 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 YQTVTFTTXNATKISYTQFIEALRAQIASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 92
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"Molecular cloning of cinnamomin A-, B-chain and the expression,
purification, characterization and mutagenesis of the A-Chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF255548; AAF68978.2; --
HSSP; P02879; 2AAI.
                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYNDOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 268 RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, ANO39011, ARKSA468.1; -.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                 Yang Q., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 YPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSN-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome_inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
Cinnamomum camphora (Camphor tree).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
VCBI_TaxID=13429;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.2%; Score 370.5; DB 10; Length 581; 48.1%; Pred. No. 9e-27; tive 25; Mismatches 57; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GESFSFB8FBA3D196 CRC64;
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Hydrolase; Signal; Toxin.
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                                                                                             SEQUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YQTVTFİTKKAİKISYİQFİEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 60
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                                                                                                                                                                                                                                                                                                                                   7 YPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSN-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosanthes kirilowii (Mongolian snake-gourd).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
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                                                                                                                                                                                                                  DB 10; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.4%; Score 334; DB 10; Length 289; Best Local Similarity 38.9%; Pred. No. 1.1e-23; Matches 72; Conservative 42; Mismatches 49; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.0%; Score 368.5; DB 10; Length 48.1%; Pred. No. 1.3e-26; tive 25; Mismatches 57; Indels
                                                                                                                                                   549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
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PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
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NCBI_TaxID=118182;
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Best Local
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                                          119 QLAGNIRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGE 178
                                                                    60 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng H., Wang B., Shaw P., Yeung H.;
"[Cloning and DNA sequencing of the gene encoding trichosanthin].";
I Chuan Hsueh Pao 21:42-51(1994).
-! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.
-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 INFTTAGATVQSYTNFIRAVRGRLTVLPN-------RVGLPINORFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1, Cucurbitales, Cucurbitaceae, Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.2%; Score 332; DB 10; Length 289; 38.9%; Pred. No. 1.7e-23; tive 42; Mismatches 49; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (FRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last amotation update) Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase). TRICHOSANTHIN, TCS.
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 A.A.
                                                                                                                                                                                                                                                                                               289 AA.
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PRINTS, PR00396; SHIGARICIN.
PROSITE, PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94271613; PubMed=8003348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                  179 MRTRI 183
                                                                                                                                                                             194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 IGKŘV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                        Q41216
Q41216;
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004367
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57 AELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI - - THLFTDVQNRYTFAFGGNY 114
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                                                                                                                                                                                                                                                                                                                                                        "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; Plant J. 12:1251-1260(1997).
-!- CATALYIIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh; "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi)."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 YPIINFTTAGATVQSYTNFIRAVR------GRLTVLPNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 DNLETAAGTRRESIELGPSPLDGAITSLYYDE-----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOSOME INACTIVATING PROTEIN, A CHAIN. RIBOSOME INACTIVATING PROTEIN, B CHAIN.
Sambucus nigra (European elder).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, campanulids; Dipsacales; Adoxaceae; Sambucus.

NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichosanthes sp. Bac Kan 8-98.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 563;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3ED2B6C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.22) (TRN N-91ycosidase) (Frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a 33.9%; Score 329.5; DB 1 Similarity 40.5%; Pred. No. 7.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000772; Ricin_B_lectin.
Interpro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AA; 62336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U76524; AAC15886.1; -. HSSP; P02879; 2AAI.
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141

564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                       63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-BAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                              10 INFITAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                             2. SPRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RENA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMB1, AB039324; BAA92530.1; -.
HINCEPPO, 188003924; RIP.
PEAM, PF00161; RIP.
PROSTIE; PR00365; SHIGARICIN.
PROSTIE; PS00275; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin l.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-! CATALYIC ACTIVITY: ENDOMYROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 26S RENA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AJ400822; CAC33178.1; -.
                                                                                                                                                                                            16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                 33.6%; Score 326; DB 10; Length 247; 39.6%; Pred. No. 5e-23; Live 44; Mismatches 50; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBirel. 17, Last sequence update)
11-MR-2003 (TrEMBirel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                             247 247 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02899; ZAMI.
InterPro; IPR000772; Ricin B lectin.
InterPro; IPR001574; RIP.
Flam; PF00652; Ricin B lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1. Glycosidase; Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                        72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
298
564
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                        Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=28503;
                                                                                                                                                                                                                                                                                                                                                        RI 183
                                                                                                                                                                                                                                                                                                                                                                             RV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sambucus ebulus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Leaf;
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        182
                                                                                                                                                               Query Match
                                                                                                                                                                              Best Local
                                                                                                                    NON TER
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MEDLINE=93132798; PubMed=8421313;

A Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

Thimary structure of three distinct isoabrins determined by cDNA

Structure of three distinct isoabrins determined by cDNA

T. GATALYNIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 289 RRNA.

SPECIFIC ADENOSINE ON THE 289 RRNA.

-I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; M98346; AAA32626.1; -.

EMBL; M98346; AAA32626.1; -.

EMBL; M98346; AAA32626.1; -.

EMBL; M98346; AAA32656.1; -.

EMBL; M98346; AAA3265.1; -.

EMBL; M98346; ARICARICIN.

EMBL; ROUGHS; RICI B lectin; 6.

PERM; PERM; PRO0156; RICIN; 2.

EMBL; PRO0158; RICIN; 2.

EMBL; PRO0458; RICIN; 2.
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                                                                                                                                                                                                                                                                                     115 DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                26
                                                                                                                                                             58 ELSVTLALDVTNAYVVGYRAGNSAYFFHEDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: ::||||||||||||: :||
61 RESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QYPIINFITAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSNHA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ODQVIKETTEGATSQSYKQFIEALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE 60
                                                                                                                          7 YPIINFTTAGATVQSYTNFIRAVRGR------LTVLPNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                 57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI - - THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Strepticphyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abrese, Abrus.
                                                                   25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
      DB 10; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.8%; Score 318.5; DB 10; Length 528; 43.3%; Pred. No. 7.4e-22; Live 22; Mismatches 69; Indels 15;
Query Match
33.3%; Score 323.5; DB 10; Length
Best Local Similarity 40.0%; Pred. No. 2.7e-22;
Matches 76; Conservative 38; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last seq
(TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS50231; RICIN B LECTIN, 2.
PROSITE, PS00275; SHIGA RICIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.8%
Best Local Similarity 43.3%
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 IEGEMRTRIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 İEOEVRRSLO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
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SEQUENCE
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Abrus precatorius (Indian licorice) (Crab's eye).
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SEQUENCE
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Q945S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                         EQLAGNLRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::| :|| || || :| || :| 3 || :| || 3 || :| || :| || 3 || :| || || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3 || 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
"Trichosanthas kirilowii trichosanthin precursor (TCS) gene.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GIYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                          Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AY082348; AAM22782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 317; DB 10; Length 270; 36.8%; Pred. No. 4.1e-22; tive 45; Mismatches 54; Indels 16
                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TremBlandere)
RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA; 29683 MW; 531713B754F9B769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AA
                                                                                                                                                                                                                                             270 AA.
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                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00161; RIP; 1.
PRINTS, PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                     22,
22,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative
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                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   >270
                                                                                                                               174 RVGVSİR 180
                                                                                          178 EMRTRIR 184
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                                                                                                                                                                                                                                                                                                                                                                            Fragment).
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Best Local
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Q38760;
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Matches
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AC Q3
DT 01
DT 01
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66 EVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 IKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLRDPTTVEERNRYITVELSNSERESI
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT C SPECIFIC ADENOSINE ON THE 288 RRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.
EMBL; X54912; CAA38654.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sambucus nigra (European elder).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                   Chaine."

J. Biol. Chem. 266:6848-6852(1991).

J. Biol. Chem. 266:6848-6852(1991).

J. Biol. Chem. 266:6848-6852(1991).

J. Biol. Chem. 266:6848-6852(1991).

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S.RNA-ABRIN-A IS MORE TOXIC THAN RICIN.

J. FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT PACLILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOGSIS.
                                                                                                                                                                                                                              TISSUBELDRF;

WEDLINE-DRB-01329; PubMed=2016300;

WHENDER G., Mathiesen A., Sundan A.;

"Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Plliat; LALL.
InterPro; IRRO01574; RIP.
Pram; PR00151; RIP; 1.
PRINTS; PR00196; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; ABRIN E, A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Ribosome-inactivating protein (EC 3.2.2.2) (TRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%; Score 310.5; DB 1 43.2%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q945S2;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 RIR 184
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                                                                                                                 NCBI_TaxID=3816;
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NCBI_TaxID=4202;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 NGNIVILAVDVINLYVVAFSGNANSYFF----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87
                                                                                                 proteins from Sambucus nigra leaves.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-! CATALYIC ACTIVITY: ENDOHYBOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AF409133.; AALOHI33.1; -.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Leaf;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin F.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF249280; AAN86130.1;
Hydrolase; Glycosidase.
Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 YPIINFTTAGATVQSYTNFIRAVR------GRLTVLDNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Gaps
                                                                                      "Characterization and cloning of lectins and ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sambucus nigra (European elder).
Subtaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus:
                                                                                                                                                                                                                                                                                                                                                                                                             / Match 31.7%; Score 307.5; DB 10; Length 563; Local Similarity 38.4%; Pred. No. 9.1e-21; Nes 73; Conservative 36; Mismatches 56; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 31.7%; Score 307.5; DB 10; Length 563; Local Similarity 38.4%; Pred. No. 9.1e-21; Los 73; Conservative 36; Mismatches 56; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin l precursor (RC 3.2.2.22).
                                                                                                                                                                                                                                                                                                                                                                             563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 AA.
                                                                                                                                                                                                                                             PEAM; PF00552; Ricin Blectin; 6. Pfam; PF00161; RIP; I PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2. PROSITE; PS50231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
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195 IEQEVRRSLQ 204
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                                 SEQUENCE FROM N.A.
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                                                                       Van Damme E.J.M.;
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7 YPIINFTTAGATVQSYTNFIRAVR------GRLTVLPNRVGLPINQRFILVELSNH
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1019 MVFXQYPIINFTTAGATVQS......ARFQYIEGEMRTRIRYNRRS 198
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ricin A from pICII Amino acid sequenc Ricin A chain. Un Ricin A-chain (RTA Ricin A-chain ribo Ricin A-chain RIP. Ricin A. Chain RIP. Ricin A. Chain RIP. Ricin A. Chain RIP. Ricin A. Chain RIP. Ricin A. Chain RIP. Ricin A. Chain RIP. Ricin A. Chain
SUMMARIES	AAR30722 AAB19265 AAR37290 AAR63902 AAW25136 AAW21699 AAP70838 AAP95639
DB	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Length	267 267 267 290 290 332 332 332
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554 16 AARY0827 562 10 AAP90079 576 8 AAC70326 576 18 AAW25787 576 21 AARY5892 576 21 AARY5892 576 22 AAC78301 576 22 AAC78302 576 22 AAC78302 576 24 AAC78302 576 24 AAC78302 574 8 AAP50166 574 10 AAP89570 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 11 AAR39571 574 12 AAR39571 574 11 AAR39571 574 12 AAR39571 574 11 AAR30573 574 12 AAR30573 574 13 AAR31703 574 11 AAR21703 574 11 AAR21703 575 11 AAR21703 576 12 AAR21703 577 11 AAR21703 578 11 AAR21703 578 11 AAR32986 589 13 AAR213986 589 13 AAR213986 589 15 AAR313986 589 15 AAR313986	Anti-cataract immu Ricin D. Ricinus Modified castor be Sequence of Ricinu	Castorbean ricin. Castor bean ricin Ricinus communis r	Castor bean prepro Sequence of prepro Castor bean prepro	Hlosynthetic multi Sequence of ricin- Sequence of Ricinu Preproricin, Rici	a ⁽¹⁾ a ⁽²⁾	Ricin A. Spinner. Ricin A chain (RTA Castor oil plant a R. communis agglut	Sequence of kicin Ricin agglutinin A Trichosanthin anti Amino acid sequenc Synthetic alpha-tr	Mature alpha-Trich Trichosanthin (a r Trichosanthin. Tr Trichosanthin from	υ σ ε Δ
	AAR7082 AAP9007 AAG7830 AAP70326					~	Ç		
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ALIGNMENTS

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pH; temperature; cultivation; host; soluble.
                                                                                    AAR30722 standard; Protein; 267 AA
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91GB-0003926.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                      Ricin A from pICI1102.
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N-PSDB; AAQ27876.
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08-FEB-1993
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 WVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                      Prepn. of ricin A comprises cultivating a host, including a DNA sequence which encodes ricin A, e.g. from pICII102, in a nutrient medium for an initial period at a first pH value which favours growth of the host, and cultivation the host for a further period at a pH lower than the first pH value, and opt. cooling the host during the terminal portion of the cultivation and harvesting the host during the the terminal portion. By adjusting the pH and temp, during the the terminal portion.
                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "vascular leak syndrome (VLS) inducing motif"
               Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by adjusting pH and/or temp. during cultivation to increase yield of soluble prod.
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1019; DB 13; Length 267; 100.0%; Pred. No. 5.8e-100; rive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                   (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                             Disclosure, Fig 9; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FQYIEGEMRTRIRYNRRS 198
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Matches 198; Conservative
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Best Local
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                                         Modifying the ability of a proteinaceous composition to induce a toxic effect for reducing vascular leak syndrome, comprises identifying at least one specified amino acid sequence and altering it
                                                                                                                                                                                                                                                                                                                                                                  1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                             1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                              The specification describes a method for producing immunotoxins and cytokines with a reduced ability to promote vascular leak syndrome (VLS). The immunotoxins are useful for treating graft versus host disease, non-Hodgkin's and Hodgkin's lymphoma, myeloma, metastatic lesion tumours and some type of solid tumours. The present sequence represents an immunotoxin (ricin toxin A chain) which induces VLS. The VLS-inducing motif can be mutated or deleted so that VLS is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
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                                                                                                                                                                                                                                                                                                   100.0%; Score 1019; DB 21; Length 267; 100.0%; Pred. No. S.8e-100; ive 0; Mismatches 0; Indels 0;
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                                                                                                   Example 1; Page 119-120; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR37290 standard; protein; 267 AA.
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92US-0901707
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                                                                                                                                                                                                                                                                                                                                   198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(updated)
                WPI; 2000-664922/64.
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                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                        267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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19-JUN-1992;
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09-JAN-2003
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                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                           induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SNHABELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 YDRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                           The invention covers analogues of Type I RIPs. Ricin is a Type II whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues pref. joined via a disulphide linkage to a molecule which specifically Updated on 09-JAM-2003 to add missing OS field.)

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKQYPIINFTTAGATVQSYTNFIRAVRGKLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                           cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide(s) encoding type I ribosome-inactivating proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
   type I ribosome inactivating protein - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.1%; Score 1010; DB 14; Length 267; 100.0%; Pred. No. 5.2e-99; .ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carroll SS, Studnicka GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63902 standard; protein; 267 AA.
                                                                                                                        Claim 1; Page 92; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US05348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 YIEGEMRIRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A-chain (RTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-006804/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricinus communis.
Analogues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9426910-A1
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR63902
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63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize, proRIP, ribosome inactivating protein, alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Inffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                       3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                            AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPS) described in AAR63903-R63911.

RIPS are the key components of cytotoxic therapeutic agents (GTAS), which include gene fushon products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is
                                                                                                                                                                                                                    desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                        99.1%; Score 1010; DB 16; Length 267;
100.0%; Pred. No. 5.2e-99;
ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A-chain ribosome inhibitory protein inactive precursor.
 which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW25136 standard; Protein; 290 AA.
                                               Example 3; Fig 1; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YIEGEMRTRIRYNRRS 198
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95US-0378761.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                    Matches 196; Conservative
                 therapeutic agents.
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                        267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1995;
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02-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1990;
26-JAN-1995;
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                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW25136;
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                    disease
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                                                                                                                                AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and betea units of the RIP. When
separated the two units regain activity and are capable of inactivating
cukaryotic ribosomes and hence preventing protein production. Many
different RIPS may be produced with an internal linker including
maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPS can be used in the construction of therapeutic
consist staged to specific cells such as tumour cells via the
attachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see U54869903). There is interest
the capacity to provide correct post-translational processing. However,
RIPS effectively inhibit protein synthesis in enkaryotic cells resulting
on cell death. Since the inactive RIP proteins are not cytotoxic to
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICLOMISEAARFO 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHBIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                          precursors of ribosome inactivating proteins - inactive eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                      99.1%; Score 1010; DB 18; Length 290; 100.0%; Pred. No. 5.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; Pred. No. 5.8 Matches 196; Conservative 0; Mismatches
                                                                                                            Claim 4; Column 91-94; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
152..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW21699 standard; Protein; 290 AA.
             Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIEGEMRTRIRYNRKS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
           Morgan AER,
                                   WPI; 1997-362934/33.
                                                                                                                                                                                                                                                                                                                                                                              290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proking the invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent of phibitors of eukaryotic protein synthesis. They possess a highly specific N-94ycosidaes activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 288 RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive prokip proteins make it possible to provide protein possible. The RIP can be used to make extended and improved ways not before possible. The RIP can be used to make extended conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDABAITHLFIDVQNRYIFAFGGN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
/note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inactive precursor of maize ribosome-inactivating protein - also
chimeric ribosome-inactivating protein precursors containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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100.0%; Pred. No. 5.8e-99;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Column 91-94; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                      95US-0378761.
                                                                                                                                                                                                                                                            92US-0987927.
                                                                                                                                                                                                                                                                                    90US-0535636.
95US-0378761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internal linker sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Morgan AER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-309831/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      (DOWC ) DOWELANCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 AA;
                                                                                                                                                                                                   26-JAN-1995;
                                                                                                                                                                                                                                                                                                               26-JAN-1995;
                                                                                                                                                                                                                                                         09-DEC-1992;
                                                                                                                                                                                                                                                                                          11-JUN-11990;
                                                                                 US5635384-A.
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                                                                                                                                             03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hey ID,
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ID AAP7
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AC AAP7
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                                                                                                                                                                                                                                                                                                                              123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                     38 PKOYPIINFITAGAIVOSYINFIRAVRGRLTIGADVRHEIPVLPNRVGLPINORFILVEL
                                                                                                                                                                                                                                                                                    3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
                                                                                                                                                                     N\text{-}terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                              Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                    Query Match
99.1%; Score 1010; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 7e-99;
Matches 196; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                               Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70838 standard; protein; 332 AA.
                                                                                                                                Chang S,
                                                                                                                                                                                             Disclosure; Fig. 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..32
/note="Leader"
                                                                                                                                                                                                                                                                                                                                                                                     183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                    218 YIEGEMRTRIRYNRRS 233
                                                                                       86US-0860330.
85US-0778414.
                                                                       86EP-0307242.
        Ricin A; Met-aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A protein encoded by pRA123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003 (updated)
18-FEB-1991 (first entry)
                                                                                                                               Bauer KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33..302
                                                                                                                                            WPI; 1987-110172/16.
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                             (CETU ) CETUS CORP.
                                                                                                                                                                                                                                       332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis.
                       Escherichia coli.
                                                                                                                                                       N-PSDB; AAN70152
                                                                                                                              Benbassat A,
                                                                                              20-SEP-1985;
                                                                       19-SEP-1986;
                                                                                      06-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant toxin.
                                                       22-APR-1987
                                      EP219237-A
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                     98
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtch. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70522) shows the nucleotide sequences of three plasmids contg. CDNA inserts obtd. by probing a CDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
99.1%; Score 1010; DB 8; Length 33:
Best Local Similarity 100.0%; Pred. No. 7e-99;
Matches 196; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 112pp; English.
                             315..332
/note="B-chain"
/note="A-chain"
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                                                                                                                                                                                                                                        86EP-0308877.
                                                                                                                                                                                                                                                                                                      86US-0837583
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                                                                                                                                                                                                                                                                                                                                                                                          CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-265177/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN70519
                                                                                                                                                                                                                                                                                                                                                             (CETU ) CETUS
                                                                                                                                                                                                                                     13-NOV-1986;
                                                                                                                                                                                                                                                                                               07-MAR-1986;
                                                                                                                                                                           23-SEP-1987.
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31-OCT-2002
                                                                                                             EP237676-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piatak M;
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                         Region
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ID AAP9
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97

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183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                       (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ85386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9503828-A1
                                                                                                                                       25-MAR-2003
                                                                                                                                                    31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1995.
                                                                                                                                                                                                                                                 Synthetic
                                                                                                              AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLDNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                            Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 1010; DB 10; Length 332; 100.0%; Pred. No. 7e-99; 1.ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                         Greenfield L, Nitecki D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                              Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                     Ricin A encoded by insert from plasmid pRA123
                                                                                                                       1..35
/label= leader sequence
                                                                                                          .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 14; 54pp; English.
                                                                                                                                                /label=A-chain
303..314
                                                                                                                                                                                                                                                                                                                                                                                                          Lawyer FC, Horn G,
                                                                                                                                                                                              315..332
/label=B-chain
                                                                                                                                                                        303..314
/label=linker
                                                                                                                                                                                                                                                                                                        84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
                                                                                                                                                                                                                                                                                  89EP-0201162
                                                                                                                                                                                                                                                                                                                                                        84US-0653515
13-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 196; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 AA;
                                                                      Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN91281
                                                                                                                                                                                                                                                                                                                                                                                (CETU ) CETUS
                                                                                                                                                                                                                                                                                 19-JAN-1989;
                                                                                                                                                                                                                                                                                                                    08-FEB-1984;
09-FEB-1984;
                                                                                                                                                                                                                                                                                                        08-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                        20-SEP-1984;
                                                                                                                                                                                                                                                                                                                                             07-SEP-1984;
                                                                                                                                                                                                                                                        04-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nost cells.
                                                                                                                                                                                                                                 EP335476-A.
                                                                                                                                                                                                                                                                                                                                                                                                         Gelfand D,
                                                                                                                                                                                                                                                                                                                                                                                                                      Piatak MJ;
                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                    Peptide
                                                                                                                                                                      Peptide
                                                                                                                                             Peptide
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chain
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                                                                                                                                                                                                                                                                                                                                                                                               Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The immunotoxin given in AAR70827 comprises the heavy and light chariable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from PHB19 in E. coli.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.1%; Score 1010; DB 16; Best Local Similarity 100.0%; Pred. No. 1.4e-98; Matches 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "MAb 4197X heavy chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..27
/label= Sig peptide
/note= "phoA signal sequence"
/label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549..554
/label= TAG
/note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                     AAR70827 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= RICIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148..166
/label= LINKER
218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0101329.
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                               Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 544
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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                 123 YDRLEQLAGNIRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFIIGIQMISEAARFQ 182
                                                                                                                    3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                            Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 99.1%; Score 1010; DB 10; Length 562; al Similarity 100.0%; Pred. No. 1.4e-98; 196; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                          AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus communis (caster beans).
                                                                                                                                                     183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                             460 YIEGEMRTRIRYNRRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88WO-US04238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0124735
                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN90068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1987;
                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                          01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                         WO8904839-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown EL,
                                                                                                                                                                                                                                                                     AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                    Ricin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                AAP90079
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98 SNHABLSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYFFAFGGN 157
                                        123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                      The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Proricin consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is protoolytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Ricin_B_chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                             Castor bean plant, preproricin, ricin; A chain, B chain, human immunodeficiency virus infection, HIV; toxin, antiviral agent, retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296..297
/label= HIV_protease_cleavage_site
304..565
                                                                                                                                                                                                                                                                                                                                                  Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                   Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosidase"
292..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Ricin A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                       AAG78304 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 25..565
/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                             183 YIEGEMRTRIRYNRRS 198
                                                                                                            218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2001; 2001WO-US05282.
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                           27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2001
                                                                                                                                                                                                                AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                             RESULT 1:
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63 SNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122

3 PKOYPIINFTTAGAIVOSYTNFIRAVRGRLITGADVRHEIPVLPNRVGLPINQRFILVEL 62

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Local Matches œ

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                                                                                                                                                                                                                                                                                                                                                                                                          YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's enchancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful infections, especially retroviral infections The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the problems of the problems.
                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                     27 PKQYPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                              PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                99.1%; Score 1010; DB 22; Length 565; 100.0%; Pred. No. 1.4e-98; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hence of Ricinus communis (castor bean) Ricin toxin or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70326 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..35
/note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0837583,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86EP-0308877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                              Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                   565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP237676-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP70326;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                       problem.
                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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XX XX BECT

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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The Library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70521, AAN70521, Shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.

(MaAN70523) and suitable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 SNHAELSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYYFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                     New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin, cytotoxin, hybrid protein, cell delivery, cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%; Score 1010; DB 8; Length 576; 100.0%; Pred. No. 1.5e-98; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                Disclosure; Fig 14(1-2); 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW25787 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36..302
/label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 YIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 YIEGEMRTRIRYNRKS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                           purer and soluble prods.
                                                 WPI; 1987-265177/38.
N-PSDB; AAN70526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castorbean ricin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
               Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW25787;
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218 YIEGEMRTRIRYNRRS 233

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This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a critical diphtheria toxin B-interleukin-2 gene that was expressed in ricin-diphtheria toxin B-interleukin-2 gene that was expressed in conditions involving over-production of cells bearing IL2 receptors, such as certain 7-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation of commain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the delivery of agents (e.g. therapeutic genes, toxins, detectable corporation of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a high brophinant protein, permitting reproducibility, consistency, and the precise control of composition.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 11A-B; 30pp; English.
                                              315..576
/label= B-domain
303..314
/label= Linker
315..576
                                                                                                                                                                                                                       84US-0618199.
85US-0726808.
85US-0742554.
89US-0556095.
90US-0538276.
                                                                                                                                                                     93US-0102387.
                                                                                                                                                                                                        91US-0722484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
les 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470103/43.
                                                                                                                                                                                                                                                                                                                                               (SERA-) SERAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT91638
                                                                                                                                                                   04-AUG-1993;
                                                                                                                                                                                                        27-JUN-1991;
                                                                                                US5668255-A
                                                                                                                                                                                                                       07-JUN-1984
                                                                                                                                 16-SEP-1997
                                                                                                                                                                                                                                         25-APR-1985
                                                                                                                                                                                                                                                          07-JUN-1985
                                                                                                                                                                                                                                                                           22-DEC-1989
                                                                                                                                                                                                                                                                                           14-JUN-1990
                                                                                                                                                                                                                                                                                                              04~AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                   Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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           Peptide
                                              Domain
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Matches
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                                                                                                                                                 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                         98 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                           YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                     38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                                                                       3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                           0; Gaps
99.1%; Score 1010; DB 18; Length 576;
100.0%; Pred. No. 1.5e-98;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                         183 YIEGEMRTRIRYNRRS 198
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Recombinant, hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV; cytosol; therapy; genetic defliciency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                          Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases -
                AAY55892 standard; Protein; 576 AA.
                                                                                                                                                                                                                  84US-0618199
91US-0722484.
85US-0726808.
85US-0742554.
89US-0456095.
                                                                                                                                                                                          95US-0488246,
                                                                                                                                                                                                           93US-0102387
                                                 15-FEB-2000 (first entry)
                                                                   Castor bean ricin toxin.
                                                                                                                                                                                                                                                                                                                 WPI; 1999-632431/54.
                                                                                                                                                                                                                                                                               (SERA-) SERAGEN INC.
                                                                                                                                       Ricinus communis.
                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ30663.
                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                       US5965406-A.
                                                                                                                                                                                                           04-AUG-1993;
                                                                                                                                                                                                                   07-JUN-1984;
27-JUN-1991;
                                                                                                                                                                                                                                                    22-DEC-1989;
                                                                                                                                                                                                                                   25-APR-1985
                                                                                                                                                                                                                                            07-TUN-1985
                                                                                                                                                                                                                                                                                                                                         Recombinant
                                                                                                                                                                         12-OCT-1999
                                                                                                                                                                                                                                                                                                Murphy JR;
                                 AAY55892;
RESULT 15
         AAY55892
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The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises to the binding domain of a naturally occurring protein a portion of a translocation domain of a naturally occurring protein coxin, in troxin, chiqa-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; which is non-native toxin, which translocate the third part of the third part comprises a polypeptide entity to be introduced into the cell, which is non-native cot the naturally occurring protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate invention. The hybrid molecule enables the direction of appropriate alleviate or cure the disease. The hybrid is sepecially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme alleviate or cure the accursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as thy HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as

Example 4; Fig 11; 31pp; English.

576 AA; Sequence

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        Query Match
        99.1%; Score 1010; DB 20; Length 576;

        Best Local Similarity 100.0%; Pred. No. 1.56-98;

        Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

        QY
        3 PKQYPIINFTTAGATVQSYTNFIRANGRITTGADVRHEIPVLDNRNGLPINQRFILVEL 97

        Cy
        63 SNHABLSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDABATTHLFTDVQNRYTFARGGN 122

        Db
        98 SNHABLSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDABATTHLFTDVQNRYTFARGGN 157

        Cy
        123 YDRLBQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISBAARFO 187

        Db
        158 YDRLBQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISBAARFO 217

        QY
        183 YIEGEMRTRIRYNRRS 198

        Db
        218 YIEGEMRTRIRYNRRS 233
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Search completed: February 10, 2004, 16:22:27 Job time: 33.7583 secs

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                                                                      February 10, 2004, 16:18:30; Search time 11.4485 Seconds (without alignments) 731.761 Million cell updates/sec
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Sequence 6, Ag
Sequence 74,
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1 MVPKQYPIINFTTAGATVQS......ARFQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27
Patent No. 5
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                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-218-303-16
US-08-303-16
US-08-318-793D-61
US-07-901-707-1
US-07-901-707-1
US-08-425-336-1
US-08-448-1138-1
US-08-446-360-1
US-08-646-360-1
US-08-136-389-1
US-08-136-389-1
US-08-136-389-1
US-08-136-389-1
US-08-356-786-8
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US-08-485-286-77
US-08-485-389-6
US-08-485-389-6
US-08-485-389-6
US-08-485-389-6
US-08-485-389-6
US-08-3389-6
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Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
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Result

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4 4 4 4 4 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7		Gaps
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		Length
28 342 33.6 267 1 US-0B-485-286-74 29 342 33.6 289 1 US-07-923-692C-4 31 342 33.6 289 1 US-07-923-692C-4 32 342 33.6 289 2 US-08-184-237-4 34 342 33.6 289 3 US-08-482-920-4 34 342 33.6 289 3 US-08-481-341-4 35 341.5 33.6 289 3 US-08-481-502-4 35 341.5 33.5 289 1 US-09-726-651A-4 35 342.5 32.3 250 1 US-08-378-31-15 37 329.5 32.3 250 1 US-08-378-31-15 38 323.5 31.7 251 4 US-07-901-707-6 41 312.5 30.7 255 1 US-07-981-6 42 312.5 30.7 255 1 US-09-9813-6 43 312.5 30.7 255 1 US-09-9813-6 44 312 30.6 289 3 US-08-9487-6 45 312 30.6 280 2 US-08-597-731-2	RESULT 1 US-08-218-303-16 Sequence 16, Application US/08218303 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. 5547867 Patent No. Strain Bumphendra V. APPLICANT: Fitch, John E. TITLE OF INVENTION: FERRENTATION PROCESS NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Cushman, Darby & Cushman, STREET: 1615 L Street, N.W. CITY: Washington STATE: DC. STREET: 1615 L Street, N.W. ZIP: 20036-5601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EMP C compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAPLICATION DATA: PRILING DATE: 26-FEB-1992 ATTORNEY/AGENT INFORMATION: PRICE ROALISTRATION NUMBER: US/08/218,303 FILING DATE: 26-FEB-1992 ATTORNEY/AGENT INFORMATION: PRESERENCE/DOCKET NUMBER: 16,773 RESERENCE/DOCKET NUMBER: 16,773 FELENOME: 202-802-0944 INFORMATION POR SEG ID NO. 16: SEQUENCE CHARACTERISTICS:	267 amino ac amino acid 37. linear TYPE: protein 16 Similarity 10 8; Conservativ

; 0

1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60

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NS-01-901-707-1

Sequence 1, Application US/07901707

Sequence 1, Application US/07901707

GENERAL INFORMATION:

APPLICANT: Bernhard, Susan L.

APPLICANT: Carroll, Steve F.

APPLICANT: Carroll, Steve F.

APPLICANT: Lane, Valie A.

ITILE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VITETTA, ELLEN S.
APPLICANT: VITETTA, ELLEN S.
APPLICANT: SAMALASHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, BOXANA,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROWE (VLS)
FILE REFERENCE: UTSD.603
CURRENT PELICATION NUMBER: US/09/538,873
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/126,826
EARLIER PELLING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
                                       61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                          121 GNYDRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISBAAR 180
                                                                                                                                                        61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 1019; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09538873
Patent No. 6566500
GENERAL INFORMATION:
                                                                                                                                                                                                                  181 FOYIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                              181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FQYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                            US-09-538-873-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-538-873-1
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                                                                   ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                          61 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYTFAFG 120
                                                                                                                                                      121 GNYDRLEQLAGNLRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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Best Local Similarity 100.0%; Score 1019; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC/XT/AI_Compatibles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC/XT/AT Compatibles
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word or ASCII editors
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/38,793D
FILING DATE: 08-No. 5840521-94
CLASSIFICATION NUMBER: 07/842,081
FILING APPLICATION DATA:
APPLICATION NUMBER: 07/842,081
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
APPLICATION NUMBER: 9104017.0
FILING DATE: 26-Feb-91
APPLICATION NUMBER: 9104017.0
FILING DATE: 25-Apr-91
FILING DATE: 29-Apr-91
FILING DATE: 29-Apr-91
FILING DATE: PAL-11 NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: DJB/9901/215431/TGM
TELEDHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMAN DARBY CUSHWAN
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                      US-08-338-793D-61
; Sequence 61, Application US/08338793D
; Patent No. S840521
; GENERAL INFORMATION:
    APPLICANT: Barth, Peter Thomas
; TITLE OF INVENTION: VECTOR
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                         TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
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REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                60603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-988-430-1
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APPLICANT: Better, Marc D.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 1010; DB 1; Length 267; 100.0%; Pred. No. 1.5e-110; Live 0; Mismatches 0; Indels (
            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                         STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                          FILLING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILLING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376246and, Greea E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 312,302
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEFAS: 25-3856
INPORMATION FOR ERG ID NO: 1:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07988430
Patent No. 5416202
GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bernhard, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-07-901-707-1
NUMBER OF SEQUENCES:
                                                                                                      Chicago
(: Illinois
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                                                                                                                                                                           60603
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                                                                                                                                                      COUNTRY:
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63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunocoxins Comprising Ribsome-Inactivating NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
CLASSIFICATION: 435
CLASSIFICATION: 435
RICA BAPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INPORMATION:
NAMME: NO EAST-ORDER: US 07/787,567
MANME: MASSIVE ASSOCIATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
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Chicago

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63 SNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: 169
ADDRESSE: MCANDARDEWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION DATA:
FILING DATE: 10-APR-1995
RICHARDINANDER: US/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US/07/901,707
FILING DATE: 12-MAY-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19-JUN-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEYERST INFORMATION:
NAME: MEYERST INFORMATION:
NAME: MEYERST INFORMATION:
NAME: WEGISTER OF UNBER: 31394
TELECOMMUNICATION INFORMATION:
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McAndrews, Held & Malloy, Ltd
                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 YIEGEMRTRIRYNRRS 198
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TOPOLOGY: 14--
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TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MOLECULE TYPE: protein US-08-425-336-1
                       Chicago
: Illinois
                                                                                                    60606-6402
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-488-113B-1
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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 122
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                                                                                  11022US07/200-70.P3.C2A
                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 575659
GENERAL INFORMATION
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 YIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/707-9155
TELEX: 650 380-1248
INPOREMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                       COMPUTER READABLE FORM:
Illinois
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                               MEDIUM TYPE:
                         60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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US-08-477-484B-1
            COUNTRY:
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